SEARCH REQUEST FORM

5 Scie	entific and Technical I	nformation Center	1 1
	mber 30 8 · 3 2 13 Results r Rm; 9 B 0 5	reprehensing order of the	ed.
Please provide a detailed statement of the s Include the elected species or structures, ke utility of the invention. Define any terms t	earch topic, and describe as sywords, synonyms, acronyn hat may have a special mean heet, pertinent claims, and ab	specifically as possible the subj ns, and registry numbers, and coing. Give examples or relevant	ect matter to be searched. Ombine with the concept or citations, authors, etc, if
Inventors (please provide full names):	inolds, Eri	<u></u> (,	
Earliest Priority Filing Date:* *For Sequence Searches Only* Please includappropriate serial number.			
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STAFF USE ONLY Searcher: Searcher Phone #: Searcher Location: Date Searcher Picked Up	Type of Search NA Sequence (#) AA Sequence (#) Structure (#) Bibliographic Litigation Fulltext Patent Family	Vendors and cost STN	
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                              908470 seqs, 133250620 residues
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Listing first 45 summaries
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1 QMEAEXIXXXEEIVPNXVEQK 21
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Anticariogenic pho	Casein phosphopept	Sequence Of Casein	Bos alpha-sl-casel	Anticariogenic pho	Casein phosphopept	Sequence of casein	Alpha-sl-casein la	Phosphopeptide 1.	Phosphopeptide 1.
	QI	AAR28426	AAR32928	AAR47815	AAW66599	AAR28433	AAR32935	AAR47822	AAR64162	AAP71320	AAR31237
	DB	13	14	15	19	13	14	15	16	œ	14
	Length	21	21	21	21	37	37	37	192	21	21
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	Score	78	7.8	7.8	7.8	7.8	7.8	7.8	78	75	75
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Phosphopeptide der	SOGIUM CASETUACE C	Anticariogenic pho		Seguence of casein	ide	Phosphopeptide #1	Anticariogenic pho	Casain phosphopept	rieser to comment		Casein derived pro	n)	•	B. burgdorferi ant	B. burgdorferi ant	$\overline{}$	Drosophila melanog		,	ם נ	מ	s .	s.		Arabidopsis thalia	polype	Human cancer assoc	Human Ovarian anti		U)	Drosophila melanog	U,	į	2	ie thali	to chart	S Clidit
AAR32308		AAR28429	AAR32931	AAR47818		200777	AADO0430	AAR26430	η.	AAR47819	ABB77538	AAR64163	AAW66605	AAY19923	AAV19922	ABB9303	ADD 5000	Appropria	ABB65643	AAG22800	AAG46524	AAG22799	AAG46523	AAG22798	AAG46522	~	AAB43831	ABP41543	ABB48886	AAG15925	C3107ggk	101010144 01010144	AAGTST40	AAY81551	2	364	AAG36208
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ALIGNMENTS

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/note= "post-translationally phosphorylated serine"
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                                                                                                                                                                                                                                                     _note= "post-translationally phosphorylated serine"
                                                                                         Casein; metal ion; dietectic; purification; growth medium; dietary supplement; fertiliser.
                                                                                                                                                 _note= "may be Glu or pyro Glu"
                                                                                                                              Location/Qualifiers
               AAR28426 standard; peptide; 21 AA.
                                                                              Anticariogenic phosphopeptide.
                                                                                                                                                                                                                                                                                                                       92WO-AU00175.
                                                          19-MAR-1993 (first entry)
                                                                                                                                    Key
Modified-site
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                                       AAR28426;
RESULT 1
         AAR28426
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The sequences given in AAR32927-35 are casein phosphopeptides which can be used to inhibit dental calculus. These peptides are pref. in the form of salts selected from alkaline metal, alkaline earth metal salts such as Na, Ca, Zn, Cu, Al, K, Sr, Mg and Ni salts. These peptides are pref. present as a Zn/phosphopeptide complex or aggregate. these peptides have anti-calculus potential, and are anti-caries and anti-
                                                                                                                                                                             Controlling dental calculus by treating teeth with oral compsns. which contains phospho-peptide(s) having 5-40 amino-acyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Casein phosphopeptide; dentinal hypersensitivity; therapy; tooth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treatment of dentinal hypersensitivity - using casein, component of casein, phospho-protein or phospho-peptide or their salts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                          94.0%; Score 78; DB 14; Length 21 76.2%; Pred. No. 1.7e-08; Ive 0; Mismatches 5; Indels
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/note= "See also residures 8,9,10,17"
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                                                                                  (VICT-) VICTORIAN DAIRY IND AUTHORITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR47815 standard; peptide; 21 AA.
                                                                                                                                                                                                                                             Claim 3; Page 16; 23pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 76.2
Matches 16; Conservative
                                                                 (UYME ) UNIV MELBOURNE
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                                    22-AUG-1991;
                                                                                                                 Reynolds EC;
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                                                                                                                                                                                                                                                            The peptide may be prepd. by completely digesting casein in soln. with a proteolytic enzyme, adding mineral acid to the soln. to addinst the pH to 4.7, removing any precipitate, adding calcium schoride to cause aggregation of the peptides in soln. and of the phosphopeptides. This method allows prodo of the phosphopeptides. This method allows prodn has anticariogenic activity and may be used as a dietectic. The puptide may be used in a microbiological growth medium, as a dietary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                           Selected phospho-peptide(s) prodn. having anticariogenic activities etc. - comprises digesting soluble monovalent cation salt of casein in soln., introducing di- or trivalent metal ion and filtering through filter having mol. wt. exclusion limit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Casein; phosphopeptide; dental calculus; salts; alkaline metal; alkaline earth metal; Zn/phosphopeptide complex; aggregate; anti-caries; anti-gingivitis.
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0
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Pred. No. 1.7e-08;
0; Mismatches 5; Indels
                              (UZME ) UNIV MELBOURNE. (VICT-) VICTORIAN DAIRY IND AUTHORITY.
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                                                                                                                                                                                                                          Claim 11; Page 10; 18pp; English.
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76.28;
   91AU-0005706
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nes 16; Conservative
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                                                                                                            WPI; 1992-382039/46.
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19-APR-1991;
                                                                                Reynolds EC;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                         casein; calcium phosphate complex; amorphous calcium phosphate; ACP; phosphopeptide; delivery vehicle; calcium fluoride; calcium deficiency; osteoporosis; osteomalacia; tooth; bone disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a stable calcium phosphate complex including phosphopeptide stabilised amorphous calcium phosphate (ACP) or its
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stable calcium phosphate complex including phospho:peptide stabilised amorphous calcium phosphate - useful for treatment of dental caries, calcium malabsorption and bone diseases such as
                                    post-translationally phosphorylated serine. A mixture of
phosphopetides (CPP) and/or their salts may be used in a
for treating dentinal hypersensitivity. Pref. those CPPs
the sequence -Ser(P) Ser(P)-Ser(P) - predominate. The CPPS
                                                                                                                                                               .
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                                                                                                                                     Score 78; DB 15; Length 21; Pred. No. 1.7e-08; 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                       Bos alpha-s1-casein X-5P (f59-79) phosphopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYME ) UNIV MELBOURNE.
(VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                         can be extracted from a casein digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                 Disclosure; Page 12; 23pp; English.
                                                                                                                                                                                                                                                                                AAW66599 standard; peptide; 21 AA.
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76.2%;
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mes 16; Conservative
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                                                                                                                     Sequence
                                                                                                                                             Query Match
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                                                                    method
                                                       casein
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purpose continuous of the proper present of the property of the present of the property of a specifically claimed complex.
derivative, where the phosphopeptide includes the amino acid sequence: Ser(P)-Ser(P)-Glu-Glu. The amorphous phases stabilised by the phosphopeptides are a delivery vehicle for co-localisation of Ca, P and phosphate at the tooth surface in a slow-release amorphous producing superior anticaries efficacy over prior art. The amorphous phases stabilised by the phosphopeptides are also useful as dietary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Casein; metal ion; dietectic; purification; growth medium; dietary supplement; fertiliser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Selected phospho-peptide(s) prodn. having anticariogenic activities etc. - comprises digesting soluble monovalent cation salt of casein in soln., introducing di- or trivalent metal ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.0%; Score 78; DB 19; Length 21; 76.2%; Pred. No. 1.7e-08; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR28433 standard; peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anticariogenic phosphopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QMEAESISSSEEIVPNSVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91AU-0005706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYME ) UNIV MELBOURNE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Sequence
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                                                                                                                                               Matches
                                                                                                                                                                                                      RESULT 7
                                                                                                                                                                                                             AAR47822
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                       with a proteolytic enzyme, adding mineral acid to the soln. to adjust the pH to 4.7, removing any precipitate, adding casein in soln. to closus aggregation of the peptides in soln. and separating the aggregation of the peptides in soln. and of the phosphopeptide by industrial methods. This method allows prodn. has anticariogenic activity and may be used as a dietectic. The supplement or as a fertiliser.

See also AAR28425-32.
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                Casein; phosphopeptide; dental calculus; salts; alkaline metal; alkaline earth metal; Zn/phosphopeptide complex; aggregate; anti-caries; anti-gingivitis.
                                                                                                                                                     .;
0
and filtering through filter having mol. wt. exclusion limit
                                                                                                                                      Length 37;
                                                                                                                                 94.0%; Score 78; DB 13; Length 37 76.2%; Pred. No. 3.3e-08; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYME ) UNIV MELBOURNE.
(VICT-) VICTORIAN DAIRY IND AUTHORITY.
               Claim 11; Page 14-5; 18pp; English.
                                                                                                                                                                                                                                                                                                                                              'label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                             'label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                             'label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                            label= Phophoserine
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                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                   AAR32935 standard; Protein; 37
                                                                                                                                                                1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                          17 QMEAESISSSEEIVPNSVEQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91US-0748344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92WO-AU00441
                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                       Local Similarity 76.2
les 16; Conservative
                                                                                                                                                                                                                                                                  Casein phosphopeptide #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-093685/11.
                                                                                                                   37 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reynolds EC;
                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                   Sequence
                                                                                                                                  Query Match
                                                                                                                                                                                                                                   AAR32935;
                                                                                                                                               Matches
                                                                                                                                                                                                      RESULT 6
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The sequences given in AAR32927-35 are casein phosphopeptides which can be used to inhibit dental calculus. These peptides are pref. in the form of Salts selected from alkaline metal, alkaline earth metal salts such as Na, Ca, Zn, Cu, Al, K, Sr, Mg and Ni salts. These peptides are pref. present as a Zn/phosphopeptide complex or aggregate. these peptides have anti-calculus potential, and are anti-caries and anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Controlling dental calculus by treating teeth with oral compsns. - which contains phospho-peptide(s) having 5-40 amino-acyl residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Casein phosphopeptide; dentinal hypersensitivity; therapy; tooth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ser(P) = post-translationally phosphorylated serine. A mixture of casein phosphopetides (CPP) and/or their salts may be used in a method for treating dentinal hypersensitivity. Pref. those CPPs contg. the sequence -Ser(P)-Ser(P)-Ser(P)- predominate. The CPPS can be extracted from a casein digest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               94.0%; Score 78; DB 14; Length 37; 76.2%; Pred. No. 3.3e-08; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= ser(P)
/note= "see also AAs 6,22,24,25,26,33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of casein phosphopeptide (CPP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (VICT-) VICTORIAN DAIRY IND AUTHORITY.
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                                                                                                               Claim 3; Page 21; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR47822 standard; peptide; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QMEAEXIXXXEEIVPNXVEQK 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 QMEAESISSSEEIVPNSVEQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYME ) UNIV MELBOURNE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 16; Conserv
                                                                                                                                                                                                                                                                                                                                   gingivitis agents.
                                                                                                                                                                                                                                                                                                                                                                                          37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Modifled-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Length 37;

DB 15;

94.0%; Score 78;

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/label= phosphoserine
                                                           'label= phosphoserine
                                                                              'label= phosphoserine
                       Location/Qualifiers
                                                                                                                                                                                                                                                              WPI; 1987-362707/51.
                                                                                                                                                                                                                         (REYN/) EC REYNOLDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphopeptide 1.
                                                                                                                                                                                                                                                                                                                                                               21 AA;
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
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                                 Modified-site
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                                                                     Modified-site
                                                                                                                                                                     12-JUN-1987;
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                                                                                                                                                                                      12-JUN-1986;
                                                                                                                                                                                                                                              Reynolds EC;
                                                                                                                                   WO8707616-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
       Synthetic
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR31237;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caries; gingivitis; periodontal disease; osteoporosis; osteomalacia.
                                                                                                                                                                                                                                                                                                                                              DNA encoding a food protein with Phe codon(s) omitted or replaced with codon(s) for other metabolisable amino acids · used to form edible polypeptide for use in nutrition for phenylketonuria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                            The sequence of cattle alpha-1-casein, lacking phenylalanine residues, and with an additional N-terminal methionine (to permit translation) is given in AAR64162. The encoding gene was designed for optimal expression in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.0%; Score 78; DB 16; Length 192; 76.2%; Pred. No. 2.3e-07; ive 0; Mismatches 5; Indels
         Indels
                                                                                                                                                               Alpha-s1-casein; phenylalanine; phenylketonuria; food;
76.2%; Pred. No. 3.3e-08; ative 0; Mismatches 5;
                                                                                                                                             Alpha-s1-casein lacking Phe residues
                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig. 15; 90pp; English
                                                                                         AAR64162 standard; Protein; 192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP71320 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QMEAEXIXXXEEIVPNXVEQK 21
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                                      17 QMEAESISSSEEIVPNSVEQK 37
                                                                                                                                                                                                                                                94WO-GB01046
                                                                                                                                                                                                                                                                 93GB-0010472
                                                                                                                                                                                                                                                                                                                      WPI; 1995-022798/03.
N-PSDB; AAQ75411; AAQ75412.
                            1 OMEAEXIXXXEEIVPNXVEQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAY-1991 (first entry)
                                                                                                                            03-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Conservative
          Conservative
                                                                                                                                                                         Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                    (UYWA-) UNIV WARWICK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
 Best Local Similarity
                                                                                                                                                                                                                                                                                                      Mann NH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphopeptide 1.
                                                                                                                                                                                                                                                16-MAY-1994;
                                                                                                                                                                                                                                                                  20-MAY-1993;
                                                                                                                                                                                                            W09428126-A.
                                                                                                                                                                                                                              08-DEC-1994
           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerevisiae
                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                                                                                                                      Carr NG,
                                                                                                           AAR64162;
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           Matches
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ID AAP7
XX
AC AAP7
XX
XX
DT 07-N
XX
XX
XX
KW Cari
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                                                                        RESULT 8
                                                                                  AAR64162
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Phosphopeptide; active agent; oral; composition; anionic; polymeric; stabiliser; carboxylate; polymer; sulfonate; destabilisation; fluoride; carles; gingivitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New phosphopeptides contg. defined aminoa cid sequence - useful in treatment of dental, rarefying bone diseases and disease relating to malabsorption of minerals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The phosphopeptide is used in compsns. at a conc. of 0.01\mbox{-}5 see also AAP71321-P71324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Match 90.4%; Score 75; DB 8; Length 21; Local Similarity 71.4%; Pred. No. 6.6e-08; les 15; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                       (VICT-) VICTORIA DAIRY INDUSTRY AUTHORITY. (UYME-) UNIVERSITY OF MELBOURNE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Phosphoserine
9
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/label= phosphoserine
                                             /label= phosphoserine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 17; 22pp; English.
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/label= OTHER
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Modified-site
                                                                                                                                                               09-AUG-1991;
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                                                                                                                           03-JUL-1992;
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                                                                                      24-FEB-1993
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                                                   EP528458-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAR31237-42 represent phosphopeptides which were used as the active agents in an oral composition. These peptides were stabilised by an anionic polymeric stabiliser. The anionic polymers were chosen from a group consisting of carboxylate polymers, sulfonate polymers, polymers having both a carboxylate as sulfonate moiety, and other such mixtures. The anionic polymeric stabiliser inhibits destabilisation of the phosphopeptide in the oral environment. These oral compositions, pref. containing a fluoride source may be used for inhibiting caries and gingivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Oral compsns. contg. a phospho:peptide - with addn. of an anionic polymeric stabiliser to inhibit destabilisation in the oral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "post-translationally phosphorylated"
17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dental; teeth; tartar control; brushite; calcium phosphate; hydroxyapatite; mouthwash; toothpaste.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.4%; Score 75; DB 14; Length 21 71.4%; Pred. No. 6.6e-08; Live 1; Mismatches 5; Indels
   /label= Phosphoserine
                                       /label= Phosphoserine
                                                                          /label= Phosphoserine
                                                                                                                                                                                                                                                                                                                          Burger AR, Elliott DL, Schick LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR32308 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 13; 18pp; English.
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                                                                                                                                                                                                                                                               (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-019802/03
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les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 AA;
                   Modified-site
                                                       Modified-site
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Modified-site
                                                                                                                                                                                        03-JUL-1992;
                                                                                                                                                                                                                            17-JUL-1991;
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                                                                                                                                                     20-JAN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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THE HEAT SAN AND SAN A
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Phosphopeptide; tryptic digestion; sodium caseinate; alpha(s1)-caseinate; phosphostrine; phosphotyrosine; phosphotyrosine; phosphohistidine; supersition; mannitol; xylltol; lactitol; cellobiitol; confectionary; carbitol; calcium; remineralisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tryptic digest of casein. The peptide may be used with an anticalculus agent, e.g. alkali metal pyrophosphate, in a compsn. for controlling dental tartar. The compsn. inhibits conversion of bybrushite and amorphous calcium phosphpate into the more stable hydroxyapatite on the teeth. The compsn. is used in the form of a mouthwash, toothpaste, gel, lozenge or chewing gum, for care of the teeth and tartar control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The peptide sequence is that of a phosphopeptide prepd. from a tryptic digest of casein. The peptide may be used with an anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phospho-peptide(s) for dental tartar control - are included in compsns. With pyrophosphate(s) or zinc salts to provide good inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
/note= "post-translationally phosphorylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.4%; Score 75; DB 14; Length 21 71.4%; Pred. No. 6.6e-08; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sodium caseinate tryptic phosphopeptide T1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR68936 standard; Peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 11; 17pp; English.
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                                                                                                                                                                                                                                            91GB-0017315
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                                                                                                                                                                                                                                                                                                                                                                                                Burger AR, Schick LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See also AAR32309-12.
                                                                                                                                                                                                                                                                                                   (UNIL ) UNILEVER PLC (UNIL ) UNILEVER NV.
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The peptide may be prepd. by completely digesting casein in soln. with a proteolytic enzyme, adding mineral acid to the soln. to adjust the pH to 4.7, removing any precipitate, adding calcium chloride to cause aggregation of the peptides in soln. and separating the aggregation of the peptides. This method allows prodn. the phosphopeptide by industrial methods. The phosphopeptide of the phosphopeptide activity and may be used as a dietectic. The peptide may be used in a microbiological growth medium, as a dietary supplement or as a fertiliser.
  /note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Casein; phosphopeptide; dental calculus; salts; alkaline metal; alkaline carth metal; Zn/phosphopeptide complex; aggregate; anti-caries; anti-gingivitis.
                                                                                                                                                                                                                                                                                                                             selected phospho-peptide(s) prodn. having anticariogenic activities etc. - comprises digesting soluble monovalent cation salt of casein in soln., introducing di- or trivalent metal ion and filtering through filter having mol. wt. exclusion limit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 73; DB 13; Length 21;
Pred. No. 1.6e-07;
1; Mismatches 5; Indels
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                                                                                                                                                                                                                   (VICT-) VICTORIAN DAIRY IND AUTHORITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 12; 18pp; English.
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                                                                                                                              92WO-AU00175
                                                                                                                                                                 91AU-0005706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 71.4
Matches 15; Conservative
                                                                                                                                                                                                         (UYME ) UNIV MELBOURNE
                                                                                                                                                                                                                                                                                                     WPI; 1992-382039/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AA;
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Modified-site
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                                                                                                                                                                       9-APR-1991;
                                                                                                                                16-APR-1992;
                                                                                                                                                                                                                                                                  Reynolds EC;
                                                       WO9218526-A.
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                                                                                           29-OCT-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha(s1) and alpha(s0). The peptides contain the amino acids phosphoserine, phosphothreonine, phosphotyrosine or phosphohistidine, and include in their sequence asparate and glutemate. The phosphopeptides form part of a novel composition containing the peptide dispersed uniformly in a crystal mix of sugars chosen from sorbitol, mannitol, xylitol, lactitol, cellobitol or mixtures of sorbitol/mannitol or sorbitol/xylitol. The compositions can be used instead of conventional sugars to manufacture confectionary products. The phosphopeptides are known to inhibit caries and gingivitis and can act as a source of calcium ions to promote/enhance remineralisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides (AAR68936-40) are phosphopeptides resulting from the tryptic digestion of sodium caseinate. The peptide shown here is derived from the TCPK-tryptic digest of alpha(s1).caseinate (comprising alpha(s1) and alpha(s0)). The peptides contain the amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "post-translationally phosphorylated serine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Casein; metal ion; dietectic; purification; growth medium; dietary supplement; fertiliser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                    Crystalline poly:ol compositions for use in confectionery and pharmaceuticals - contain a phospho:peptide uniformly distributed within the crystal matrix and can improve oral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.4%; Score 75; DB 16; Length 21; 71.4%; Pred. No. 6.6e-08; tive 1; Mismatches 5; Indels
            /note= "Phosphoserine"
                                                                     /note= "Phosphoserine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; column 4; 8pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR28429 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anticariogenic phosphopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EMEAESISSSEEIVPNSVEOK 21
                                                       /label- OTHER
                                                                                                                                                                                     94EP-0304083.
                                                                                                                                                                                                                          93US-0078706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Conservative
                                                                                                                                                                                                                                                                (ICIL ) ICI AMERICAS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            WPI; 1995-044845/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-1993
                                                                                                                                                                                           07-JUN-1994;
                                                                                                                                                    21-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                         Duross JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                              hygiene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Gaps

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                                                                                                                                                                                                                              The sequences given in AAR32927-35 are casein phosphopeptides which can be used to inhibit dental calculus. These peptides are pref. in the form of salts selected from alkaline metal, alkaline earth metal salts such as Na, Ca, Zn, Cu, Al, K, Sr, Mg and Ni salts. These peptides preperting as 2n/phosphopeptide complex or aggregate. These peptides have anti-calculus potential, and are anti-caries and anti-
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                       Controlling dental calculus by treating teeth with oral compsns. which contains phospho-peptide(s) having 5-40 amino-acyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Casein phosphopeptide; dentinal hypersensitivity; therapy; tooth.
                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                         Length 21;
                                                                                                                                                                                                                                                                                                                                   88.0%; Score 73; DB 14; Length 21 71.4%; Pred. No. 1.6e-07; Live 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Ser(P)
/note= "see also residues 8,9,10,17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of casein phosphopeptide (CPP).
                                                                                                            (VICT-) VICTORIAN DAIRY IND AUTHORITY
   /label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYME ) UNIV MELBOURNE. (VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR47818 standard; peptide; 21 AA.
                                                                                                                                                                                                            Claim 3; Page 18; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     1 OMEAESISSSEEIVPDSVEOK 21
                                                                                                                                                                                                                                                                                                                                                                        1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                 91US-0748344.
                                                              92WO-AU00441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93WO-AU00319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92AU-0003221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.4
Matches 15; Conservative
                                                                                                  (UYME ) UNIV MELBOURNE.
                                                                                                                                                  WPI; 1993-093685/11.
                                                                                                                                                                                                                                                                                                                 21 AA;
                                                          21-AUG-1992;
                                                                               22-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Modified-site
                                                                                                                                 Reynolds EC;
                   WO9303707-A
                                        04-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-1992;
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                                                                                                                                                                        Ser(P) = post-translationally phosphorylated serine. A mixture of casein phosphopeptides (CPP) and/or their salts may be used in a method for treating dentinal hypersensitivity. Pref. those CPPs contg. the sequence -Ser(P)-Ser(P)-Ser(P)- predominate. The CPPs can be extracted from a casein digest.
                                                                   component
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                              Treatment of dentinal hypersensitivity - using casein, composof casein, phospho-protein or phospho-peptide or their salts
                                                                                                                                                                                                                                                                                                                                                                                    88.0%; Score 73; DB 15; Length 21; 71.4%; Pred. No. 1.6e-07; Live 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: February 11, 2003, 18:16:53 Job time : 32.5258 secs
                                                                                                                          Disclosure; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QMEAESISSSEEIVPDSVEOK 21
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 71.4 Matches 15; Conservative
WPI; 1994-025888/03.
                                                                                                                                                                                                                                                                                                                                   21 AA;
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sequence 4, Applia
sequence 2, Applia
sequence 2, Applia
sequence 4, Applia
sequence 4, Applia
sequence 4037, Applia
sequence 5, Applia
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                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 2, Appli
                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, sequence 5, sequence 5, sequence 5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9,
Sequence 9,
Sequence 5,
Sequence 5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                           February 11, 2003, 18:14:31; Search time 10.3918 Seconds (without alignments) 59.459 Million cell updates/sec
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                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
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US-08-954-985A-9
US-08-137-086-9
US-08-137-086-5
US-08-137-086-5
US-08-137-086-6
US-08-954-985A-6
US-08-954-985A-6
US-08-985A-6
US-08-137-086-6
US-08-137-086-6
US-08-138-138-1
US-08-110-5
        Compugen Ltd
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US-08-137-086-2
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                                                                                                                                                                               Total number of hits satisfying chosen parameters:
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compug
                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                               262574 seqs, 29422922 residues
                                                                                                                                                                                                                               Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
                                                                                                                1 OMEAEXIXXXEEIVPNXVEOK 21
                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
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Match Length DB
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37
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Maximum DB seq length: 2000000000
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83
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76.5
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                                                                                                                                                                              Searched:
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sequence 51, Appl

US-08-994-570-5 US-08-975-762-51 US-09-295-028-51

Sequence 51,

Seguence 5,

US-09-092-458-2 US-09-021-560-4 US-09-134-001C-4037 US-09-134-309A-5

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                                                                                                                                                        Sequence 12, Sequence 12, Sequence 12, 1
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Sequence 2, sequence 13,
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                                               Sedneuce
                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: REYNOLDS, ERIC CHARLES FOR THE TITLE OF INVENTION: PHOSPHOPEPTIDES FOR THE TITLE OF INVENTION: TREATMENT OF DENTAL CALCULUS NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: STARKE & SAWALL CORRESPONDENCE ANDRES, SCEALES, STARKE & SAWALL ADDRESSEE: SUITE 1100 EAST WISCONSIN AVE., SUITE 1100 EAST WISCONSIN AVE.,
             US-09-100

US-09-068-140A-13

US-08-97-762-23

US-08-91-324-23

US-08-925-028-23

US-09-105-582-23

US-09-105-582-23

US-09-106-123

US-08-606-888A-5

US-08-606-888A-12

US-08-606-046-6

US-09-066-046-6

US-09-066-046-6

US-09-055-250

US-09-104-15

US-09-104-15
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19910822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: SARA, CHARLES 30,492
NAME: SARA, CHARLES 30,492
REGISTRATION NUMBER: C.845
REFERENCE/DOCKET NUMBER: C.845
RELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-2022
TELEPHONE: (608) 255-2182
TELEPAN: (608) 255-2182
TELEFAN: 26832 ANDSTARK
TELEX: 26832 ANDSTARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIGW TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-748-344B-2 Application US/07748344B Sequence 2, Sequence 2, Sequence 2, Patent No. 5227154 BEENGLDS, ERIC CHARLES APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Pyroglutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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APPLICATION NUMBER: US,
FILING DATE: 19910822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMINO ACID
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                          53202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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LOCATION:

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OTHER INFORMATION:
OTHER INFORMATION:
Post-translationally phosphorylated serine
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OTHER INFORMATION:
Post-translationally phosphorylated serine
                                                                                                                      OTHER INFORMATION:
OTHER INFORMATION: Post-translationally phosphorylated serine
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OTHER INFORMATION: Post-translationally phosphorylated serine
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OTHER INFORMATION: Post-translationally phosphorylated serine
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Local Similarity 76.2%; Score 78; DB 1; Length 21;
hes 16; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ii Dental School, The University of Melbourne
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2. Application US/08954985A
Patent No. 5981475
GENERAL INFORMATION:
TITLE OF INVENTION: A Treatment for Sensitive Teeth
CORRESPONDENCE 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING CONTRARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,985A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,479
FILING DATE: 22-FEB-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              1 OMEAEXIXXXEEIVPNXVEOK 21
                                                                                                                                                                                                                                                                                                                                                               NAME: WOZN, Thomas M
REGISTRATION NUMBER: 28,922
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 271-7590
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett.
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Victoria
: Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: /11 L-CTTY: Melbourne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                               US-08-954-985A-2
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0; Gaps
                                                                     LOCATION: 6
OTHER INFORMATION: Post-translationally phosphorylated serine
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                         OTHER INFORMATION: A Certain amount will exist in this form
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Sequence 2, Application US/08137086

Patent No. 6448374

GENERAL INFORMATION:

APPLICANT: REYNOLDS, ERIC CHARLES

TITLE OF INVENTION:

TITLE OF INVENTION:

PRODUCTION OF PHOSPHOPEPTIDES FROM CASEIN
                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 76.2%; Score 78; DB 2; Length 21;
Matches 16; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL STREET: 100 EAST WISCONSIN AVE., SUITE 1100 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: FLOPPY DISK
COMPUTER: TBM PC COMPATIBLE
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
FILING DATE: US/08/137,086
CLASSIFICATION: 530
PRIOR ADDITION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JMBER: US/08/137,086
04-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.8493-87
NAME/KEY: Pyroglutamate
                                                         NAME/KEY: Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNATION NUMBER: 30.492
REGISTRATION NUMBER: 30.492
REFERENCE/DOKET NUMBER: 30.492
TELEPIONE: (608) 255-202
TELEFAX: (608) 255-202
TELEFAX: (608) 255-202
TELEFAX: 2632 ANDSTARE
INFORMATION FOR SEQ ID NO: 255-202
SEQUENCE CHARACTERISTICS: 2632 ANDSTARE
                                                                                                                                                                           NAME/KEY: Phosphoserine
                                                                                                                                                                                                                                     NAME/KEY: Phosphoserine
                                                                                                                                                                                                                                                                                              NAME/KEY: Phosphoserine
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TITLE OF INVESTIGATOR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY ;
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                       US-08-954-985A-2
                                                                                                                                                                                                                                                                                                               LOCATION:
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RESULT 5
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                                                                                                                                              LOCATION: 1
TOTHER INFORMATION:
OTHER INFORMATION: A certain amount will exist in this form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: REYNOLDS, ERIC CHARLES
TITLE OF INVENTION: PHOSPHOPEPTIDES FOR THE
TITLE OF INVENTION: TREATMENT OF DENTAL CALCULUS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: 9
ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL
STREET: 100 EAST WISCONSIN AVE., SUITE 1100
CITY: MILMAUKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/748,344B
FILING DATE: 19910822
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/07748344B
Patent No. 5227154
GENERAL INFORMATION:
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                                                                                                                   NAME/KEY: Pyroglutamate
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                 Amino acid
EDNESS: single
                                                                                MOLECULE TYPE: Protein
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                                                              linear
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                                          STRANDEDNESS:
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US-07-748-344B-9
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CORRESPONDENCE ADDRESS:
STREET: 711 Elizabeth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 94.0%; Score 78; DB 1; Length 37; Best Local Similarity 76.2%; Pred. No. 1.7c-08; Matches 16; Conservative 0; Mismatches 5; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: A Treatment for Sensitive Teeth
NUMBER OF SEQUENCES: 9
                                                                                   C.8493-87
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                                        ALTONALIS SARA, CHARLES S NAME: SARA, CHARLES S REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: C. 845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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FILING DATE: ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                    TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Protein
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OTHER INFORMATION:
US-07-748-3448-9
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NAME/KEY: Phosphoserine
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APPLICATION NUMBER:
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                                                                                                    MILWAUKEE
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                                                                                                                                   COUNTRY:
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                                                                                                    OPERATING C. SCTURE SCTURE ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,985A
                                                                                                                                                                                                                                                                                                      322-00033
                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,479
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
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US-08-137-086-9
Sequence 9, Application US/08137086
Setatent No. 6448374
GENERAL INFORMATION:
APPLICANT: REYNOLDS, ERIC CHARLES
                                                                                                                                                                                                                                                              NAME: WOZNY, Thomas M
REGISTRATION NUMBER: 28,922
REFERENCE/DOCKET NUMBER: 327
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                        TELEPHONE: (414) 271-7590
TELEFAX: (414) 271-5770
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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NAME/KEY: Phosphoserine
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                                                                                Diskette
                                                          COMPUTER READABLE FORM:
Melbourne
: Victoria
RY: Australia
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TOPOLOGY: Linear
                                                                    MEDIUM TYPE: D.
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Best Local Similarity
Matches 16; Conserve
                            COUNTRY: 1
ZIP: 3000
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TITLE OF INVENTION: PRODUCTION OF PHOSPHOPEPTIDES FROM CASEIN NUMBER OF SCUUNCES.

CORRESONGENCE ANDRESS.

CORRESONGENCE ANDRESS.

COURTER: 100 ANDRESS.

COURTER: WISCONSIN AVE., SUITE 1100

COUNTWILL STAD AND ASSET WISCONSIN AVE., SUITE 1100

COUNTWILL STAD AND ASSET WISCONSIN AVE., SUITE 1100

COURTRESS WISCONSIN COUNTRIES.

COUNTRIES THESE POCEAN

MANEY COUNTRIES.

COUNTRIES WISCONSINC POST-TRANSLATIONALLY PROPROPORTIONAL COUNTRIES.

COUNTRIES WISCONSINC POST-TRANSLATIONAL PROPROSETIONAL COUNTRIES.

COUNTRIES WISCONSINC POST-TRANSLATIONAL PROPROSETIONAL COUNTRIES.

COUNTRIES WISCONSTANCE.

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FEATURE:
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                                                               ;
0
                        Length 37;
                      94.0%; Score 78; DB 4; Length 37; 76.2%; Pred. No. 1.7e-08; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                         STREET: MORUS. SCEALES, STARKE & SAWALL STREET: 100 EAST WISCONSIN AVE., SUITE 1100 CITY: MILWAUKRE STATE: WISCONSIN COUNTRY: USA ZIP: FOR STATE: USA
                                                                                                                                                                                                                          US-07-748-344B-5
| Sequence 5, Application US/07748344B
| Patent No. 5227154
| CENERAL INFORMATION:
| APPLICANT: REFNOLDS, ERIC CHARLES
| TILE OF INVENTION:
| TILE OF INVENTION: TREATMENT OF DENIAL CALCULUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.8493-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/748,344B
FILING DATE: 19910822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30,492
                                                                                                                             17 QMEAESISSSEEIVPNSVEQK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IEEEPHONE: (608) 255-2022
TELEFAX: (608) 255-2182
TELEFX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                         1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Phosphoserine
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                          Query Match
Best Local Similarity 76.2%
Matches 16; Conservative
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19910822
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
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                                                  Post-translationally phosphorylated serine
                                                                                                                  Ouery Match 88.0%; Score 73; DB 1; Length 21; Best Local Similarity 71.4%; Pred. No. 8.2e-08; Matches 15; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: REYNOLDS, Eric Charles
APPLICANT: REYNOLDS, Eric Charles
TITLE OF INVENTION: A Treatment for Sensitive Teeth
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dental School, The University of Melbourne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08,362,479
FILING DATE: 22-FEB-1995
ATTORNEY/ACENT INFORMATION:
NAME: WOZDY, Thomas M
REGISTRATION NUMBER: 28,922
REFERENCE/DOCKET NUMBER: 322-00033
TELEPHONE: (414,271-7590
TELEPHONE: (414) 271-7590
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/954,985A
FILING DATE: 21-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 5, Application US/08954985A; Patent No. 5981475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM
OPERATING SYSTEM: Windows 95
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Melbourne
                                                                                                                                                                                                                    1 QMEAEXIXXXEEIVPNXVEQK 21
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NAME/KEY: Phosphoserine
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MEDIUM TYPE: Diskett
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                   LOCATION: 17
OTHER INFORMATION:
OTHER INFORMATION:
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TOPOLOGY: Linear
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                                                                                        US-07-748-344B-5
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OTHER INFORMATION: Post-translationally phosphorylated serine
                                                                                                           LOCATION: 17
OTHER INFORMATION: Post-translationally phosphorylated serine
                                                                                                                                                                                                      88.0%; Score 73; DB 4; Length 21; 71.4%; Pred. No. 8.2e-08; tive 1; Mismatches 5; Indels
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/748,344E
                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 6, Application US/07748344B
; Patent No. 5227154
                                                                                                                                                                                                                                                                                                  1 QMEAESISSSEEIVPDSVEQK 21
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(608) 255-2182
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                                                                                            NAME/KEY: Phosphoserine
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                   Best Local Similarity 71.49
Matches 15; Conservative
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TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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CITY: MILWAUKEE
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STRANDEDNESS: SIR
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                   LOCATION:
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US-08-137-086-5
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                                                                           FEATURE:
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; LOCATION: 17
; OTHER INFORMATION: Post-translationally phosphorylated serine US-08-954-985A-5
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                                                                                                                                                                                                                                                                                                                             APPLICANT: REYNOLDS, ERIC CHARLES
TITLE OF INVENTION: PRODUCTION OF PHOSPHOPEPTIDES FROM CASEIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Post-translationally phosphorylated serine
                                                                       88.0%; Score 73; DB 2; Length 21; 71.4%; Pred. No. 8.2e-08; tive 1; Mismatches 5; Indels
                                                                                  Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL STREET: 100 EAST WISCONSIN AVE., SUITE 1100 CITY: MILWAUKEE STATE: WISCONSIN COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,086
FLING DATE: 04-MAR-1994
CLASSIPICATION: 530
PROGR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.8493-87
                                                                                                                                                                                                                                                    US-08-137-086-5; Sequence 5, Application US/08137086; Patent No. 6448374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30, 492
REFERENCE/DOCKET NUMBER: C.84
TELECOMMUNICATION INFORMATION:
                                                                                                                                              1 OMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                     1 QMEAESISSSEEIVPDSVEQK 21
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TELEFAX: (608) 255-2182
TELES: 26832 ANDSTARK
TELES: 26832 ANDSTARK
SEQUENCE CHARACTERISTICS:
                                                                 Ouery Match
Best Local Similarity 71.4*
Matches 15; Conservative
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TOPOLOGY: linear
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OTHER INFORMATION: Post-translationally phosphorylated serine
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APPLICANT: REYNOLDS, ERIC CHARLES
TITLE OF INVENTION: PHOSPHOPEPTIDES FOR THE
TITLE OF INVENTION: TREATMENT OF DENTAL CALCULUS
                                                                  NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL
STREET: 100 EAST WISCONSIN AVE., SUITE 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: C.8493-87
TELECOMMUNICATION INFORMATION:
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ADDRESSEE:
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LOCATION:
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      LOCATION:
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                                                                                                                                                                                                                                                                                         84.3%; Score 70; DB 1; Length 21; 66.7%; Pred. No. 3.1e-07; Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dental School, The University of Melbourne STREET: 711 Elizabeth Street CITY: Melbourne STRATE: Victoria COUNTRY: Australia ZIP: 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: REYNOLDS, Eric Charles
TITLE OF INVENTION: A Treatment for Sensitive Teeth
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                            Post-translationally phosphorylated serine
                                                                                                                                                                                                                                         Post-translationally phosphorylated serine
                                                Post-translationally phosphorylated serine
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21-OCT-1997
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APPLICATION NUMBER: 08/362,479
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 28,922
REPERENCE/DOCKET NUMBER: 322-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 271-7590
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 6, Application US/08954985A
; Patent No. 5981475
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7%
Matches 14; Conservative
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Phosphoserine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2 CLASSIFICATION:
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COMPUTER: IBM
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                                                                                                                                                                            ) OTHER INFORMATION: Post-translationally phosphorylated serine US-08-954-985A-6
                             OTHER INFORMATION: Post-translationally phosphorylated serine
                                                                                                    LOCATION: 10 OTHER INFORMATION: Post-translationally phosphorylated serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: REYNOLDS, ERIC CHARLES
TITLE OF INVENTION: PRODUCTION OF PHOSPHOPEPTIDES FROM CASEIN
                                                                                                                                                                                                                                                  84.3%; Score 70; DB 2; Length 21; 66.7%; Pred. No. 3.1e-07; Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: ANDRUS, SCEALES, STARKE & SAWALL 100 EAST WISCONSIN AVE., SUITE 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: C.8493-87
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08137086 Patent No. 6448374
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(608) 255-2182
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NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAR-1994
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
                                                                                                                                                           Phosphoserine
                                                                              NAME/KEY: Phosphoserine
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NAME/KEY: Phosphoserine
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                  Best Local Similarity 66.79
Matches 14; Conservative
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: MILWAUKEE
STATE: WISCONSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07/959,951
                                                                                                                                                                                                                                                                                                                       ; Sequence 5, Application US/08340011
; Patent No. 5776755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08901710
Patent No. 6107046
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
                   STRANDEDNESS: single
                                                                                                                                                                                       1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                             1 QMEAEXI-XXEEIVPNXVEQK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meyers, Thomas C. REGISTRATION NUMBER: 36,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/95
FILING DATE: 09-0CT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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Best Local Similarity 46.7.
Matches 7; Conservative
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MOLECULE TYPE: peptide
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                                                                       US-09-443-339A-1
                                                                                                                                                                                                                                                                                 RESULT 14
US-08-340-011-5
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                                                                                                                                                                                                                                                                                                                                                         Query Match

84.3%; Score 70; DB 4; Length 21;
Best Local Similarity 66.7%; Pred. No. 3.1e-07;
Matches 14; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09443339A
Patent No. 6391849
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: AVI Shamay et al.
TITLE OF INVENTION: METHOD AND A PHARMACEUTICAL
COMPOSITION FOR DISRUPTING
LACTATION IN A MANMARY GLAND AND
FOR TREATING MASTITIS
               Post-translationally phosphorylated serine
                                                                                                             Post-translationally phosphorylated serine
                                                                                                                                                                                                       Post-translationally phosphorylated serine
                                                                                                                                                                                                                                                                                                     Post-translationally phosphorylated serine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Word for Windows version 2.0 converted to an ASCI file
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/443, 339A
FILING DATE: 19-No. 6391849-1999
CLASSIFICATION: <URNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Virginia COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 818/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
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SEQUENCE CHARACTERISTICS:
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                       Phosphoserine
                                                         Phosphoserine
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                 FEATURE:
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FEATURE:
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Query Match 76.5%; Score 63.5; DB 4; Length 20; Best Local Similarity 95.2%; Pred. No. 5.2e-06; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                            Satent No. 57,00,50
GENERAL INFORMATION:
APPLICANT: Alitalo, et al.
TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
TITLE OF INVENTION: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.4%; Score 36; DB 1; Length 1311;
46.7%; Pred. No. 1e+02;
tive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  3: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,011
FILING DATE:
CLASSIFICATION: 435
```

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APPLICANT: Appelikova, Olga
APPLICANT: Arisation, Natita
APPLICANT: Arisation, Elia
APPLICANT: Arisation, Elia
APPLICANT: Arisation, Maja-Tertu
APPLICANT: Mathainen, Arja-Tertu
APPLICANT: Mathainen, Arja-Tertu
APPLICANT: Mathainen, Maja-Tertu
APPLICANT: Mathainen,
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GenCore version 5.1.3

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2003, 18:19:51; Search time 10.1753 Seconds (without alignments)

52.729 Million cell updates/sec

Title: US-09-380-738A-1

Perfect score: 83-09-380-738A-1

Sequence: 1 OMEAEXIXXXEEIVPNXVEQK 21

Scoring table: BLOSUM62

Scoring table: DADSUM62
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Total number of hits satisfying chosen parameters: 140
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

140259 segs, 25548876 residues

Searched:

Published_Applications_AA:*

| cgn2_6/ptodata/2/pubpaa/US0B_NEW_DUB.pep:*
| cgn2_6/ptodata/2/pubpaa/DS0B_NEW_DUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_DUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_DUB.pep:*
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| l3: / cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| l4: / cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 1276, Ap	Seguence 37733, A	Sequence 524, App	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 14, Appl	Sequence 16, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 5358, Ap	Sequence 12523, A	Sequence 10892, A	Sequence 2, Appli	Sequence 3, Appli	Sequence 51, Appl	Sequence 51, Appl	Sequence 2, Appli	Sequence 13, Appl
	QI	US-09-925-301-1276	US-09-864-761-37733	US-09-925-297-524	US-10-029-382-2	US-09-391-340-4	US-09-948-369-4	US-09-948-369-14	US-09-948-369-16	US-10-034-849-2	US-10-034-621-2	US-09-815-242-5358	US-09-815-242-12523	US-09-815-242-10892	US-08-834-666A-2	US-09-738-877-3	US-09-159-469-51	US-09-798-042-51	US-09-800-528-2	US-09-800-528-13
	DB	10	10	10	jo	10	10	10	10	12	12	10	10	10	ω	10	10	10	10	10
	Query Match Length DB	766	253	374	803	803	803	803	803	803	803	1213	1217	305	708	1781	125	125	162	173
e)(P	Query Match]	44.6	42.2	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	8 0 5	30.8	30.8	38.6	38.0	38.6	38.6
	Score	37	. K	34	7 ° °	3.4	3.4	3.4	34	34	34	3.4	34		3.0	3.6	3.5	3.5	32	32
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Sequence 23, Appl Sequence 23, Appl Sequence 164, Appl Sequence 7, Appli	ra ara		sequence 552, App Sequence 4, Appli Sequence 494, Appl Sequence 494, App Sequence 6, Appl Sequence 6, Appli
US-09-159-469-23 US-09-798-042-23 US-09-734-569-164 US-10-046-961-7			US-10-007-805-5 US-10-045-815-4 US-10-076-622-49 US-10-007-805-4 US-10-045-815-6 US-10-076-622-47
10 10 9	-		0000
233 233 303 424	445 445 445 445 466	4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	736 736 743 743 747 1002
32 32 32 32	32222		0000000 000000
20 21 22 23	24 22 24 28 29 29	20 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	: 2044444 2010842

ALIGNMENTS

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Sequence 3773, Application US/09864761
; Sequence 372020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David R.
; APPLICANT: Chen, Renshaud R.
; APPLICANT: Chen, Renshaud R.
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó;
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                                                        GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: Palo6
CURRENT FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: PCT/0500/05882
PRIOR APPLICATION NUMBER: PCT/0500/05882
PRIOR FILING DATE: 1909-03-18
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
           ; sequence 1276, Application US/09925301
; Patent No. US20020052308A1
                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       ), ORGANISM: Homo sapiens
US-09-925-301-1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
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US-09-864-761-37733
US-09-925-301-1276
                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1276
LENGTH: 766
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TYPE: PRT
ORGANISM: Homo sapiens
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Matches 6; Conseru
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404 KELVPNRVER 413
                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 524
LENGTH: 374
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LENGTH: 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
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OTHER INFORMATION: EXPRESSED IN HBLA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HEAL, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEARY, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HEARY, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUGN, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
OTHER INFORMATION: SYRESYED IN BRAIN, SIGNAL = 2.8
OTHER INFORMATION: SYRESYED IN BRAIN, SIGNAL = 2.8
OTHER INFORMATION: SYRESYED IN BRAIN, SIGNAL = 2.8
OTHER INFORMATION: SWISSPROT HIT: P30414, EVALUE 1.00e-108
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 37733
LENGTH: 253
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PELICATION NUMBER: US 60/180,312
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-3
PRIOR FILING DATE: 2000-06-3
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-3
PRIOR FILING DATE: 2000-09-3
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00661
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00670
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00667
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
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; Sequence 524, Application US/09925297
; Patent No. US20020081659A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-09-21
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Best Local Similarity
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Sequence 2, Application US/10029382
Patent No. US20020164618A1
GENERAL INFORMATION
APPLICANT: DIVERSA CORPORATION
APPLICANT: CALLEN, Walter
APPLICANT: MATHUR, Eric
TITLE OF INVENTION: ENZYMES HAVING HIGH TEMPERATURE POLYMERASE ACTIVITY AND METHOD
TITLE OF INVENTION: THERROF
FILE REFERENCE: DIVER1350-2
CURRENT APPLICATION NUMBER: US/10/029,382
CURRENT FILING DATE: 2001-12-21
PRIOR PILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
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LOCATION: (77)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-297-524
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APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA.105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PATENTION OF 2.0
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US-09-391-340-4
; Sequence 4, Application US/09391340A
; Patent No. US20020013455A1
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SOFTWARE: PatentIn version 3.0
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Matches 11; Conservative
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APPLICANT: DIVERSA CORPORATION:
APPLICANT: CALLEN, Walter
APPLICANT: CALLEN, Walter
TITLE OF INVENTION: ENZYMES HAVING HIGH TEMPERATURE POLYMERASE ACTIVITY AND METHO
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF ILLY DATE: 2001-09-06
CURRENT FILLS DATE: 2001-09-06
CURRENT FILLS DATE: 2000-09-06
PRIOR APPLICATION NUMBER: US 09/556,309
PRIOR FILING DATE: 1999-09-07
PRIOR FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: US 08/907,166
PRIOR APPLICATION NUMBER: US 08/907,166
NUMBER OF SEQ ID NOS: 16
SEQ ID NOS: 16
SEQ ID NOS: 16
SEQ ID NO 60-
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Sequence 2, Application US/10034849;
Patent No. US20020115108A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: MATHUR, Eric
TITLE OF INVENTION: BNZYMES HAVING HICH TEMPERATURE POLYMERASE ACTIVITY
TITLE OF INVENTION: THEREOF;
TITLE OF INVENTION: THEREOF;
FILE REFERENCE: DIVER1350-2
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Pred. No. 90;
3; Mismatches 1; Indels
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Pred. No. 90;
3; Mismatches 1
CURRENT APPLICATION NUMBER: US/09/948,369
CURRENT FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US 09/656,309
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 1999-09-07
PRIOR FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: US 08/907,166
PRIOR PILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PETCHIN VETSION 3.0
SOFTWARE: 9803
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ilarity 60.0%;
Conservative
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Best Local Similarity 60.v.
6, Conservative
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404 KELVPNRVER 413
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404 KELVPNRVER 413
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Matches 6; Conserv
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US-10-034-849-2
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APPLICANT: DIVERSA CORPORATION
APPLICANT: DIVERSA CORPORATION
APPLICANT: CALLEN, WAITER
APPLICANT: MATHUR, ELIC
TITLE OF INVENTION: ENZYMES HAVING HIGH TEMPERATURE POLYMERASE ACTIVITY AND METHODS
FILE OF INVENTION: THEREOF
FILE REFERENCE: DIVER1350-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09948369;
Patent No. US2002013224341
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: CALLEN, Walter
APPLICANT: APTICANT: EXAMENCE FILE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
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                                  APPLICANT: Callen, Walter
APPLICANT: Callen, Walter
APPLICANT: Callen, Walter
APPLICANT: Mather, Eric
TITLE OF INVENTION: ISOLATION AND IDENTIFICATION OF NOVEL POLYMERASES
FILE REFERENCE: 09010/027001
CURRENT APPLICATION NUMBER: US/09/391,340A
CURRENT FILING DATE: 1999-09-07
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0

ERGITH: 803
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Pred. No. 90;
3; Mismatches 1; Indels
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FILE REFERENCE: DIVERI350-3
CURRENT APPLICATION NUMBER: US/09/948,369
CURRENT FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US 09/656,309
PRIOR APPLICATION NUMBER: US 09/391,340
PRIOR FILING DATE: 1909-09-07
PRIOR FILING DATE: 1999-09-07
PRIOR FILING DATE: 1999-09-07
PRIOR FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VEYSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
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Best Local Similarity 60.0
Matches 6; Conservative
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404 KELVPNRVER 413
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404 KELVPNRVER 413
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                    GENERAL INFORMATION:
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US-09-948-369-4
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FILING DATE: 2000-03-21

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APPLICANT: DIVERSA CORPORATION

APPLICANT: CALLEN, Walter

APPLICANT: MATHUR, Enic

TITLE OF INVENTION: ENZYMES HAVING HIGH TEMPERATURE POLYMERASE ACTIVITY

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: DIVERL350-2

CURRENT APPLICATION NUMBER: US/10/034,621

CURRENT APPLICATION NUMBER: US/20/656,309

PRIOR APPLICATION NUMBER: US/20/656,309

PRIOR FILING DATE: 2000-09-06

SOFTWARE: PATENTIN OFF: 2000-09-06

SEQ ID NOS: 2

LENGTH: 803
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APPLICANT: 2yskind, Judith W.
APPLICANT: Wall, Maniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tammoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Prokaryotes
FILE REFRENCE: ELITRA 0.11A
FILE REPRENCE: ELITRA 0.11A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: US/10/034,849
                        CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US/09/656,309
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
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Patent No. US20020061569Al
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10034621 Patent No. US20020132997A1
                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Pyrolobus fumarius
US-10-034-849-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Pyrolobus fumarius US-10-034-621-2
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Lhag 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                   404 KELVPNRVER 413
                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                            11 EEIVPNXVEQ 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404 KELVPNRVER 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                             SEQ ID NO 2
LENGTH: 803
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                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Adselbeck, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: 2yskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: DEVOKATYOUS
TITLE OF INVENTION: 100-03-21
CURRENT APPLICATION NUMBER: 60/103,21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/203,625
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-216-61
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PESSEX FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.0%; Score 34; DB 10; Length 12
38.9%; Pred. No. 1.5e+02;
Live 3; Mismatches 8; Indels
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41.0%; Score 34; DB 10; Length 12
Best Local Similarity 38.9%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5358
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269, 308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 12523, Application US/09815242; Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 38.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-815-242-12523
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LENGTH: 1217
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APPLICANT: Watray, Richard
APPLICANT: Watson, Susan
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF ANGIOGENESIS, COMPOSITIONS, ANI
TITLE OF INVENTION: SCREENING FOR ANGIOGENESIS MODULATORS
TITLE REFERENCE: A-69806/DJB/JJB, 877
FILE REFERENCE: A-69806/DJB/JJB, 877
CURRENT FILING DATE: 2000-12-15
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 1999-08-11
PRIOR FILING DATE: 1999-08-11
PRIOR FILING DATE: 1999-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 1999-08-11
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Pred. No. 3.6e+02;
3; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 8; Length 708; Pred. No. 1.2e+02; i. Mismatches 6; Indels
                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,666A
FILING DATE: 01-APR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REGISTRATION NUMBER: 06132/038001
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3, Application US/09738877; Patent No. US20020015970A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: Signal Sequence
; LOCATION: 1...19
; OTHER INFORMATION:
US-08-834-666A-2
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37.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 39.8%;
Best Local Similarity 38.9%;
Matches 7; Conservative
                                                                                               MEDIUM TYPE: Diskette COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 39.8
Best Local Similarity 37.5
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 OMEAEXIXXXEEIVPN 16
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                                                              COMPUTER READABLE FORM:
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US-09-738-877-3
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COUNTRY: USA
                                                                                     MEDIUM TYPE:
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Patent No. US20020044949A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Lissolo, Ling
APPLICANT: Tomb, Jean-Francois
APPLICANT: All-lar, Charles
APPLICANT: Al-Garawi, Amal
TITLE OF INVENTION: 76 kDa Helicobacter Polypeptides and
TITLE OF INVENTION: Corresponding Polynucleotide Molecules
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.8%; Score 33; DB 10; Length 305; Best Local Similarity 36.8%; Pred. No. 45; Matches 7; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Haselbeck, Rouel,
APPLICANT: Oblsen, Rari L.
APPLICANT: Oblsen, Rari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramick, John D.
APPLICANT: Tramick, John D.
APPLICANT: Tramick, John D.
APPLICANT: Amamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: PROKATYOLES
TITLE OF INVENTION: DATE: 2000-03-21
FILE REFERENCE: ELIFRA.011A
CURRENT APPLICATION NUMBER: 60/206,848
FRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/255,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR 
                                                                                                                                                                                                                                        Sequence 10892, Application US/09815242 Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecalis
US-09-815-242-10892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 QVPEELLNVTDMIVPNETE 190
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                                                              134 EAENILLEQTIDEVIEQ 151
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                      3 EAEXIXXXEEIVPNXVEQ 20
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Search completed: February 11, 2003, 18:36:13 Job time : 12.1753 secs

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// cgn2_6/ptodata/1/paa/US06_COMB.ppp:*
// cgn2_6/ptodata/1/paa/US081_COMB.ppp:*
// cgn2_6/ptodata/1/paa/US081_COMB.ppp:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                               OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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83
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		Description	US-08-545-573-13 Sequence 13, Appl					
SUM		ID	-80-SD 6	-80-SD	ns-08-	ns-08-	-80-SD	00-2H V
		DB						
		Query Match Length DB	94.0 125	125	192	192	199	001
	dР	Query Match	94.0	94.0	94.0	94.0	94.0	
		Score	78	78	78	78	78	100
		Result No.		10	ım	4	· KC	

ក្រហប់ពេល១០	equence 21, Appl equence 23, Appl Sequence 11897, Sequence 28072, Sequence 28072,	equence 30821, equence 11896, equence 16363, equence 28071, equence 18243, equence 30820,	aquence 11895, aquence 16362, aquence 16362, equence 18242, equence 18242, equence 23250, equence 23250, equence 105233	Sequence 2832, Ap Sequence 2880, Ap Sequence 1366, Ap Sequence 23721, A Sequence 23721, A Sequence 18758, A Sequence 18758, A Sequence 19523, A Sequence 19523, A
10-229-066 8-545-573A 77-731-592B 09-380-738 08-545-573- 18-545-573- 18-545-573- 18-545-573-	US-08-545-573A-21 US-08-545-573A-23 US-09-708-427-1189 US-09-935-625-1636 US-09-935-625-1834	US-09-935-625-3 US-09-935-625-3 US-09-935-625-1 US-09-935-625-1 US-09-935-625-3 US-09-935-625-3	US-09-708-427-1189 US-09-935-625-1636 US-09-935-625-2807 US-09-935-625-30811 US-09-22-791-1 US-09-22-791-1 US-09-791-5375 US-00-791-5375 US-09-791-5375	US-09-614-150- US-60-161-637- US-09-570-581A US-09-614-150- US-60-191-681- US-60-191-681- US-60-191-681- US-60-191-681- US-60-191-681- US-09-791-537- US-09-791-537-
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199 214 211 211 124 124 200	200 200 1280 1280 1280	1286 1328 1328 1328 1328 1334	1396 1396 1396 1402 1402 1402 131 131	2456 4666 4666 2421 2421 2421 2687 392 530
94.0 94.0 90.4 88.0 76.5 76.5			~~~~~~~~~~	444444444 0.0.0.0.0.0.0.444 0.0.0.0.0.0.
78 78 73 73 53.5 563.5	9 9 9 6 6 6	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	,	
7 8 110 112 113 113	15 16 18 198	20 22 23 24 25 26	3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5) W W W W 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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TITLE OF INVENTION: PHENYLALANINE-FREE PROTEIN AND DNA CODING TITLE OF INVENTION: THEREFORE
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                              Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                  Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO GB94/01046
FILING DATE: 16-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/545,573
FILING DATE: 16-JAN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                            Sequence 13, Application US/08545573
GENERAL INFORMATION:
APPLICANT: CARR, N.G.
APPLICANT: MANN, N.H.
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                             STREET: TWO EMERGENCY CITY: San Francisco
                                                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       94111
                                                                                                                                                                                                       ADDRESSEE:
                 US-08-545-573-13
                                                                                                                                                                                                                                                                                 COUNTRY:
RESULT 1
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Sequence 13, Application US/08545573A
GENERAL INFORMATION:
APPLICANT: Carr, Noel Gordon
APPLICANT: Mann, Nicholas Harold
TITLE OF INVENTION: Phenylalanine-Free Protein and DNA Coding
                                                                                                                                                                                                                                                                                                                                                                            94.0%; Score 78; DB 9; Length 125; 76.2%; Pred. No. 2e-07; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                      REFERENCE/DOCKET NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 016994-011900US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 326-2400
TELEPHONE: (650) 326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
TOPOLARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      016994-011900US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/545,573A
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB94/01046
FILING DATE: 16-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9310472.7
FILING DATE: 20-MAY-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: GB 9310472.7
FILING DATE: 20-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 QMEAESISSSEEIVPNSVEQK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ 1D NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 76.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-545-573-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: TWO DAILY...
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
LOCATION: 1..125
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94111-3834
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/note= "mature bovine alpha-s1-casein with
phenylalanine residues removed and addition of
methionine residue."
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                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PHENYLALANINE-FREE PROTEIN AND DNA CODING
TITLE OF INVENTION: THEREFORE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
; OTHER INFORMATION: /note= "predicted sequence of bovine ; OTHER INFORMATION: casein block A" US-08-545-573A-13
                                                                               94.0%; Score 78; DB 9; Length 125. 76.2%; Pred. No. 2e-07; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.0%; Score 78; DB 9; Length 192; 76.2%; Pred. No. 3.6e-07; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,573
FILING DATE: 16-JAN 1996
CLASSIFICATION 435
PROOF APPLICATION DATA:
APPLICATION NUMBER: WO GB94/01046
FILING DATE: 16-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9310472.7
FILING DATE: 20-MAY-1993
ATTONNEY/AGENT INFORMATION:
NAME: TIFUS COUNTY 100:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 016994-011900US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                            US-08-545-573-9; Sequence 9, Application US/08545573; GENERAL INFORMATION:
                                                                                                                                                                                66 QMEAESISSSEEIVPNSVEQK 86
                                                                                                                                                             1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37,505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 326-2422
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (650) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: LIEBESCHUETZ, JOE
REGISTRATION NUMBER: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 192 amino acids TYPE: amino acid
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 76.2%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: TWO EMEGACOCITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                     APPLICANT: CARR, N.G. APPLICANT: MANN, N.H.
                                                                                                  Local Similarity
nes 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein
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OTHER INFORMATION:
OTHER INFORMATION:
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; OTHER INFORMATION:
US-08-545-573-9
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                                                                                 Query Match
                                                                                                                     Matches
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CORRESPONDENCE ADDRESS:
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Sequence 42, Application US/08545573A
GENERAL INFORMATION:
APPLICANT: Carr, Noel Gordon
TITLE OF INVENTION: Phenylalanine-Free Protein and DNA Coding
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                    APPLICANT: Carr, Noel Gordon
APPLICANT: Carr, Noel Gordon
APPLICANT: Garr, Noel Gordon
APPLICANT: Mann, Nicholas Harold
TITLE OF INVENTION: Phenylalanine-Free Protein and DNA Coding
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "mature bovine alpha-sl-casein with phenylalanine residues removed and addition of an N-terminal methionine residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.0%; Score 78; DB 9; Length 192; 76.2%; Pred. No. 3.6e-07; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,573A FILING DATE: 16-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        016994-011900US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB94/01046
FILING DATE: 16-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9310472.7
FILING DATE: 20-MAY-1993
ATTORIEZ/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPERENCE DOCKET NUMBER: 01699
TELECOMUNICATION INCRMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHRARCTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
                                                                                             Sequence 9, Application US/08545573A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 OMEAESISSSEEIVPNSVEOK 76
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Best Local Similarity 76.2%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                        94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 16 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-545-573A-42
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                                                                                    US-08-545-573A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
                                                                   RESULT 4
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US-09-066-330-9

US-09-066-330-9

US-09-066-330-9

Sequence 9, Application US/09066330A

Sequence 9, Application US/09066330A

GENERAL INFORMATION:

APPLICANT: Bhogal, Peter S.

APPLICANT: Slakeski, Nada

TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE

FILE REFERENCE: Reynolds

CURRENT APPLICATION NUMBER: US/09/066,330A

CURRENT FILING DATE: 1998-09-15

EARLIER APPLICATION NUMBER: PCT/AU96/00673

EARLIER FILING DATE: 1995-10-30

EARLIER FILING DATE: 1996-10-30

MUMBER OF SEQ ID NOS: 15

SEQTUARE: Patentin Ver. 2.0

SEQ ID NO 9

FENCENT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: 1..26
; OTHER INFORMATION: /note= "mature bovine alpha-sl-casein"
US-08-545-573A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.0%; Score 78; DB 9; Length 199; 76.2%; Pred. No. 3.8e-07; +ive 0; Mismatches 5; Indels
                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/545,573A FILING DATE: 16-JAN-1996 CLASSIFICATION: 435
Townsend and Townsend and Crew LLP
                        Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                016994-011900US
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB94/01046
FILING DATE: 16-MAY-1994
FILING DATE: 16-MAY-1994
APPLICATION NUMBER: GB 9310472.7
FILING DATE: 20-MAY-1993
ATTORNEY/AGRNT INFORMATION:
                                                                                                                                                                                                         16-JAN-1996
                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INCORDER: ULT TELEPHONE: (415) 576-0200 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS:
                                                                                                                                               E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 QMEAESISSSEEIVPNSVEQK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 76.29
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
                                                 San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT; ORGANISM: Bos taurus
US-09-066-330-9
                                                                    California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199
            ADDRESSEE:
                                                                                                                                                                        COMPUTER:
                                                                                         COUNTRY:
                                 STREET:
                                                                    STATE:
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APPLICANT: Reyrolds. Eric C.
APPLICANT: Bhogal, Peter S.
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
FILE REFERENCE: Reyrolds.
FILE REFERENCE: Reyrolds.
CURRENT FILING DATE: 2002-09-26
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1995-10-30
PRIOR FILING DATE: 1995-10-30
PRIOR FILING DATE: 1995-10-30
PRIOR FILING DATE: 1995-10-30
PRIOR FILING DATE: 1996-10-30
                                                                 Gaps
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Sequence 41, Application US/08545573A
GENERAL INFORMATION:
APPLICANT: Carr, Noel Gordon
TITLE OF INVENTION: Phenylalanine-Free Protein and DNA Coding
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                 ;;
0
Query Match
94.0%; Score 78; DB 14; Length 199;
Best Local Similarity 76.2%; Pred. No. 3.8e-07;
Matches 16; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.0%; Score 78; DB 26; Length 199; 76.2%; Pred. No. 3.8e-07; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB94/01046
FILING DATE: 16-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/545,573A FILING DATE: 16-JAN-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                        ; Sequence 9, Application US/10229066; GENERAL INFORMATION:
                                                                                                                            59 QMEAESISSSEIVPNSVEOK 79
                                                                                               1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 QMEAESISSSEEIVPNSVEQK 79
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.29
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Bos taurus
US-10-229-066-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                US-10-229-066-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 9
LENGTH: 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Post-translationally phosphorylated OTHER INFORMATION: serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: POSt-translationally phosphorylated OTHER INFORMATION: serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Post-translationally phosphorylated OTHER INFORMATION: serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Burger, Allan R.
APPLICANT: Elliott, David L.
APPLICANT: Schick, Laura A.
TITLE OF INVENTION: Oral Compositions Containing a
TITLE OF INVENTION: Phosphopeptide
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette-3.5 inch, 1.44 Mb storage
                                                             NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 016994-011900US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft Word(R)
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/07/731,592B
FILING DATE: 19910717
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: GB 9310472.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/07731592B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 QMEAESISSSEEIVPNSVEQK 94
                        FILING DATE: 20-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                 214 amino acids
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                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 76.23
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Phosphoserine
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                                                                                                                                                                                                                                                               TOPOLOGY: linear;
MOLECULE TYPE: protein US-08-545-573A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                               EQuence
LENGTH: 214 cm.
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 21
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 45 River
CITY: Edgewater
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PHENYLALANINE-FREE PROTEIN AND DNA CODING TITLE OF INVENTION: THEREFORE
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.0%; Score 73; DB 17; Length 21; 100.0%; Pred. No. 1.9e-07; tive 0; Mismatches 0; Indels
LOCATION: 10 OTHER INFORMATION: POSt-translationally phosphorylated OTHER INFORMATION: Serine
                                                                                                 LOCATION: 17
OTHER INFORMATION: Post-translationally phosphorylated OTHER INFORMATION: serine
                                                                                                                                                                            90.4%; Score 75; DB 3; Length 21; 71.4%; Pred. No. 7.4e-08; 71.4%; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: REYNOLDS, ETIC
APPLICANT: REYNOLDS, ETIC
TITLE OF INVENTION: CALCIUM PHOSPHOPEPTIDE COMPLEXES
FILE REPERENCE: 040268/0161
CURRENT APPLICATION NUMBER: US/09/380,738A
CURRENT APPLICATION NUMBER: PCT/AU98/00160
PRIOR APPLICATION NUMBER: PCT/AU98/00160
PRIOR FILING DATE: 1998-03-13
PRIOR FILING DATE: 1998-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COTHER INFORMATION: Xaa is a phosphorylated Serine US-09-380-738A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (9)..(9)
OTHER INFORMATION: Xaa is a phosphorylated Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (6)..(6)
OTHER INFORMATION: Xaa is a phosphorylated Serine
NAME/KEY: misc_feature
LOCATION: (8)..(8)
OTHER INFORMATION: Xaa is a phosphorylated Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa is a phosphorylated Serine
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                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/09380738A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 OMEAEXIXXXEEIVPNXVEOK 21
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                                                                                                                                                                                                                                                                                             1 OMEAEXIXXXEEIVPNXVEQK 21
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SOFTWARE: Patentin version 3.0
SEQ ID NO 1.2
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 21; Conservative
                                                                          NAME/KEY: Phosphoserine
                                                                                                                                                                                                 Ouery Match
Best Local Similarity 71.4
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: (10)..(10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Bos sp.
                                                                                                                                                                                                                                                                                                                                                                                                   US-09-380-738A-1
                                                                                                                                                           US-07-731-592B-1
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Sequence 15. Application US/08545573A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wann, Nicholas Harold
TITLE OF INVENTION: Phenylalanine-Free Protein and DNA Coding
TITLE OF INVENTION: Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.5%; Score 63.5; DB 9; Length 124; 71.4%; Pred. No. 0.00019; Live 0; Mismatches 5; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                  DEFOLIX TYPE: Floppy disk
COMPUTER: IBM PC COMPAILBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Two Embarcadero Center, Eighth Floor
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            016994-011900US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/545,573A
FILING DATE: 16-JAN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                       APPLICATION DATA:
APPLICATION NUMBER: WO GB94/01046
FILING DATE: 16-WAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9310472.7
FILING DATE: 20-WAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/545,573
FILING DATE: 16-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 QMEAESISSSEEIVPNS-EQK 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (650) 326-2400
TELERAX: (650) 326-2422
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: LIEBESCHUETZ, JOE
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.5%
Query Match
Best Local Similarity 71.4%
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO -545-572-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two cancers CITY: San Francisco canarg: California
                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                           California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                        FILING DATE: 16
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                USA
                                                                                                                                                94111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-545-573-15
                                                                                                               STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
                                                                                                                                                        ; MOLECULE TYPE: protein US-08-545-573-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 68 1%
Best Local Similarity 66.7%
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94111
                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-545-573-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-545-573-23
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PHENYLALANINE-FREE PROTEIN AND DNA CODING TITLE OF INVENTION: THEREFORE NUMBER OF SEQUENCES: 37 CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
76.5%; Score 63.5; DB 9; Length 124;
Best Local Similarity 71.4%; Pred. No. 0.00019;
Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COCATION: 1..124

COTHER INFORMATION: /note= "actual sequence obtained for OTHER INFORMATION: bovine casein block A"

US-08-545-573A-15
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COMPUTER: IBM PC compatible
OPERATION PSTATION PC-DOS/MS-DOS
SOFTWARE: PATHLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:

APPLICATION NUBBER: WO PCT/GB94/01046
FILING DATE: 16-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUBBER: GB 9310472.7
FILING DATE: 20-MAY-1993
ATTORNEY/GEBTE INFORMATION:
NAME: LiebesChuetz, Joe
REGISTRATION NUMBER: 37,505
REGISTRATION NUMBER: 37,505
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPA: (415) 576-0300
TELEPA: (415) 576-0300
TELEPA: (415) 576-0300
SEQUENCE CHARACTERISTICS:
TENCTH: 124 amino acids
                                                                                                                                                                                                                      016994-011900US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and rownsend constructions STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         016994-011900US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO GB94/01046
FILING DATE: 16-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION DATA: GB 9310472.7
APPLICATION NUMBER: GB 9310472.7
ATGNERS/AGENT INFORMATION:
NAME: LIBESCHUET', JOE
REGISTRATION NUMBER: 37,505
REGISTRATION NUMBER: 37,505
RECISTRATION NUMBER: 37,505
RECISTRATION NUMBER: 016994-0119
TELEPHONE: (650) 326-2400
TELEPHONE: (650) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/545,573
FILING DATE: 16-JAN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-545-573-21
US-08-545-573-21
S Gquence 21, Application US/08545573
S GENERAL INFORNATION:
APPLICANT: CARR, N.G.
APPLICANT: MANN, N.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 QMEAESISSSEEIVPNS-EQK 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                      linear
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1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MANN, N.G.
APPLICANT: MANN, N.G.
TITLE OF INVENTION: PHENYLALANINE-FREE PROTEIN AND DNA CODING
TITLE OF INVENTION: THEREFORE
NUMBER OF SEQUENCES: 37
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                             68.1%; Score 56.5; DB 9; Length 200; 66.7%; Pred. No. 0.0097; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.1%; Score 56.5; DB 9; Length 200; 66.7%; Pred. No. 0.0097; Live 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,573 FILLIG DATE: 16-JAN-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               016994-011900US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO GB94/01046
FILING DATE: 16-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9310472.7
FILING DATE: 20-MAY-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/08545573 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     66 QNEAESISSSEEIVPNS-EQK 85
                                                                                                                                                                                                                                           1 QMEAEXIXXXEEIVPNXVEQK 21
2. LERISTICS:
TYPE: anino acids
TOPDLOGY: 1:-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (650) 326-2100
TELEFAX: (650) 326-2422
INFOREMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 QNEAESISSEEIVPNS-EOK 85
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                                                                                                                                                                                Best Local Similarity 66.73
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: LIEBESCHUETZ, JOE REGISTRATION NUMBER: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 amino acids
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1; Gaps
                 Sequence 21, Application US/08545573A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mann, Nicholas Harold
TITLE OF INVENTION: Phenylalanine-Free Protein and DNA Coding
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
TOWNERS OF SEQUENCES: 43
CORRESPONDENCE ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.1%; Score 56.5; DB 9; Length 200; 66.7%; Pred. No. 0.0097; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "combined sequence of bovine
casein blocks A and B"
                                                                                                                                                                                                                                                                                                                                                            CAPUTE: 94.11.730.34
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-05/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,573A
FILING DATE: 16-JAN-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB94/01046
FILING DATE: 16-MAY-1994
PRIOR APPLICATION NUMBER: WO PCT/GB94/01046
FILING DATE: 16-MAY-1994
PRIOR APPLICATION NUMBER: GB 9310472.7
FILING DATE: 20-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  016994-011900US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTONIOLIA MARIE: LIEDESCHUELZ, JOE REGISTRATION NUMBER: 37,505 REGISTRATION NUMBER: 01699 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200 INFORMATION FOR SED ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 200 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QMEAEXIXXXEEIVPNXVEQK 21
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Best Local Similarity 66.74
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein LOCATION: 1.200 OTHER INFORMATION: COTHER INFORMATION: US-08-545-573A-21
                                                                                                                                                                                                                                                                                                                                 X: USA
94111-3834
RESULT 15
US-08-545-573A-21
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Sequence 82477, A Sequence 824877, A Sequence 82483, A Sequence 82489, A Sequence 82489, A Sequence 82496, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 82495,
                                                                                         (without alignments)
72.734 Million cell updates/sec
                                                                          February 11, 2003, 18:17:56; Search time 24.0309 Seconds
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                            Pending_Patents_NA_New:*

1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-724-676-82495
US-09-724-676A-82494
US-09-724-676-82493
US-09-724-676-82493
US-09-724-676-82493
US-09-724-676-82499
US-09-724-676-82498
US-09-724-676-82498
US-09-724-676-82498
US-09-724-676-82477
US-09-724-676-82489
US-09-724-676-82489
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US-09-724-676-82489
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US-09-724-676A-82496
US-09-724-676A-82497
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US-10-293-017-56
US-10-293-071-56
US-10-165-193A-9
                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                420401 segs, 83231269 residues
                                                                                                                                                                                                                                                                                                                                         Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
                                                                                                                                                               1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
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Match Length DB
                                                                                                                              US-09-380-738A-1
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1302
1302
1336
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Sequence 2, Appl
Sequence 2, Appl
82475, A
82476, A
82476, A
82481, A
82481, A
82481, A
82482, A
82482, A
82486, A
82486, A
82486, A
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8, Appli
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Sequence 381, App
Sequence 17, Appl
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46.7%; Pred. No. 4.3;
Live 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.4%; Score 36; DB 5; Length 96; 46.7%; Pred. No. 4.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 82488, Application US/09724676A; Sequence 82488, Application US/09724676A; GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing; FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNBER: US/09/724.676A
CURRENT FILING DATE: 2000-11-28
SOFTWARE: PATENTIN NOS: 97222
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 82488
LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variants of alternative splicing
    US-09-724-676-82475
US-09-724-676-82476
US-09-724-676-82475
US-09-724-676-82481
US-09-724-676-82481
US-09-724-676-82482
US-09-724-676-82482
US-09-724-676-82487
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US-09-949-002-381
US-10-287-218-17
US-09-949-002-381
US-10-288-148-8
US-10-288-148-8
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; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
   TITLE OF INVENTION: Variants of alternative
; FILE REFERENCE: 129181.4 Compugen
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 9722
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82488
; LENTH: 96
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Best Local Similarity 46.,
7; Conservative
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              ORGANISM: Homo sapiens
US-09-724-676A-82488
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US-09-724-676-82488
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Matches 7; Conserv
                   RESULT 1
US-09-724-676-82488
                      Query Match
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2 MEAEXIXXXEEIVPN 16

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46.7%; Pred. No. 5.4;

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Best Local Similarity 46.7'
Matches 7; Conservative
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US-09-724-676-82493
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46.7%; Pred. No. 5.4;
Ative 2; Mismatches 6; Indels
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46.7%; Pred. No. 5.4;
tlve 2; Mismatches 6; Indels
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                                                                                                                 APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REPERENCE: 122181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 82495
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
FILE REPERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT PILIOR DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SEQ ID NO SEQ 10 NOS: 97222
SEQ ID NO 82494
                                                                                    ; Sequence 82494, Application US/09724676
; GENERAL INFORMATION:
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Best Local Similarity 46.7'
Matches 7; Conservative
 43 MSLERIKTFEELLPN 57
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hes 7; Conservative
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US-09-724-676-82494
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US-09-724-676-82495
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US-09-724-676A-82494
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43.4%; Score 36; DB 5; Length 117;
Best Local Similarity 46.7%; Pred. No. 5.4;
Matches 7; Conservative 2; Mismatches 6; Indels
    6; Indels
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 1291014. Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 82495
LENGTH: 117
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN VERSION 3.2
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TITLE OF INVENTION: Variants of alternative splicing
FILE REPERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
2; Mismatches
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; Sequence 82495, Application US/09724676A
; GENERAL INFORMATION:
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Best Local Similarity 46.7
                                 2 MEAEXIXXXEEIVPN 16
                                                                   1 MSLERIKTFEELLPN 15
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US-09-724-676A-82495
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ORGANISM: Homo sapiens
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US-09-724-676-82477
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LENGTH: 1265
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46.7%; Pred. No. 8;
tive 2; Mismatches 6; Indels
                                                       Score 36; DB 5; Length 161;
Pred. No. 8;
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                    APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERRNCE: 129101.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT APPLICATION NUMBER: US/09/724,676A
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 82392
LENGTH: 161
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                                                               43.48;
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Best Local Similarity 46...
T; Conservative
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Best Local Similarity 46.7.
Conservative
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                                                                                                Conservative
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43 MSLERIKTFEELLPN 57
                                                                                                                                   2 MEAEXIXXXEEIVPN 16
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US-09-724-676A-82492
            ; ORGANISM: Homo sapiens US-09-724-676-82493
                                                                             Best Local Similarity
Matches 7; Conserv
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US-09-724-676A-82493
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TYPE: PRT
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46.7%; Pred. No. 99;
tive 2; Mismatches 6; Indels
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46.7%; Pred. No. 98;
tive 2; Mismatches 6; Indels
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46.7%; Pred. No. 98;
tive 2; Mismatches 6; Indels
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TITLE OF INVENTION: Variants of alternative splicing
TITLE REPERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 82477
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATERIN VETSION 3.2
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NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PALENTIN VERSION 3.2
SEQ ID NO 82498
LENGTH: 1265
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                  Db 1220 MSLERIKTFEELLPN 1234
                                                                                                                                                                           Query Match 43.4
Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 MEAEXIXXXEEIVPN 16
                                                                                                                                                                                                                                                  2 MEAEXIXXXEEIVPN 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens US-09-724-676A-82498
                                                                                                                    ORGANISM: Homo sapiens
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Matches 7; Conserv
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43.4%; Score 36; DB 5; Length 1274;
Best Local Similarity 46.7%; Pred. No. 99;
Matches 7; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
43.4%; Score 36; DB 5; Length 1280;
Best Local Similarity 46.7%; Pred. No. 99;
Matches 7; Conservative 2; Mismatches 6; Indels
                APPLICANT: Compugen LTD:
TITLE OF INVENTION: Variants of alternative splicing
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 82477
LENGTH: 1274
TYPE: PRT

CORGANISM: Homo sapiens
US-09-724-676A-82477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 82483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 1242 MSLERIKTFEELLPN 1256
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; GENERAL INFORMATION:
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Search completed: February 11, 2003, 18:35:17 Job time : 25.0309 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 11, 2003, 18:14:11; Search time 18.4021 Seconds Run on:

(without alignments)
109.706 Million cell updates/sec

1 QMEAEXIXXXEEIVPNXVEQK 21 **BLOSUM62** Perfect score: Sednence:

US-09-380-738A-1

Title:

Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

pir1:* pir2:* pir3:* pir4:* PIR_73:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	a-s1-	alpha-s1-casein pr	-s1-	m		CD.	l pr	×	α.				hypothetical prote	oit	IMP-E2 protein pre	hypothetical prote	hydrolase, ama/hip	<u>ظ</u> .	DNA polymerase I	DNA polymerase I [(1)		hypothetical prote		ď	hypothetical prote			conserved nypormer
	B ID	1 KABOSB					-		2 T19384				2 T10627									1 A45661	D95		2 AI1707	2 B86901	2 T38253	8099	A425	ပ္ပ
	Length DB	214		214										113															396	5
ф	Query Match I			α	v	65.1	3	53.0	6		7		7	ď			44.6	4	. 4	. 4		43.4	43.4	43.4	43.4	· Cr	3		42.8	42.2
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	precursor
m	ha-sl-casein
OSB	ha

RESULT 1

C;Species: Bos prinigenius taurus (cattle) C;Date: 24-Apr-1984 #sequence_revision 06-Feb-1995 #text_change 21-Jul-2000 C;Accession: S22575; A23071; S02202; A90940; A91188; A91192; A91274; S23156; A90738; R;Koczan, D.; Hobom, G.; Seyfert, H.M. Nucleic Acids Res. 19, 5591-5596, 1991

A; Title: Genomic organization of the bovine alpha-S1 casein gene. A; Reference number: \$22575; MUID:92051301; PMID:1658736 A; Accession: \$22575 A; MUID:92051301; PMID:1658736 A; Status: translation not shown

A; Molecule type: DNA A; Residues: 1-214 <KOC>

A; Cross-references: EMBL:X59856; NID:g91; PIDN:CAA42516.1; PID:g92
R; Stewart, A.F.; Willis, I.M.; Mackinlay, A.G.
Nucleic Acids Res. 12, 3895-3907, 1984
A; Title: Nucleotide sequences of bovine alpha-s1- and kappa-casein cDNAs. A; Reference number: A93517; MuID:84221403; PMID:6328443
A; Accession: A23071

A:Molecule type: mRNA A;Residues: 1-214 <STE> A;Residues: 1-214 <STE> A;Residues: 1-214 <STE> A;Cross-references: GB:X00564; NID:g175; PIDN:CAB57792.1; PID:g6015490 B;Gorodetskii, S.I.; Zakharyev, V.M.; Kyarshulite, D.R.; Kapelinskaya, T.V.; Skryab: B;Gorodetskii, S.I.; Zakharyev, V.M.; Kyarshulite, D.R.; Kapelinskaya, T.V.; Skryab: B;Gorodetskii, S.I.; Zakharyev, V.M.; Kyarshulite, D.R.; Kapelinskaya, T.V.; Skryab: A;Title: Cloning and nucleotide sequence of cDNA for bovine alpha(SI)-casein. A;Reference number: S02202

A; Residues: 1-142,'D', 144-210,'IS',213-214 <GOR>
A; Residues: 1-142,'D', 144-210,'IS',213-214 <GOR>
A; Cross-references: EMBL:M3641
A; Note: this paper is a translation of the Russian paper published in Biokhimiya (1')
A; Note: the authors translated the codon CAA for residue 74 as Glu, GAG for residue
R; Mercier, J.C.; Grosclaude, F.; Ribadeau-Dumas, B.
Eur. J Biochem. 40, 323, 1973
A; Title: Structure primaire de la caseine alpha-si et de la caseine beta bovine.
A; Title: Structure primaire de la Caseine alpha-si et de la Caseine beta bovine.
A; Reference number: A01214; MUID:74082245; PMID:4797901
A; Contents: annotation; A, B, C, and D variants, revisions to positions 74 and 92-97.
B; Willis, I.M.; Stewart, A.F.; Caputo, A.; Thompson, A.R.; Mackinlay, A.G.

A;Title: Construction and identification by partial nucleotide sequence analysis of A;Reference number: A90940; MUID:83182023; PMID:6897774 A;Accession: A90940

A; Molecule type: mRNA A; Residues: 55-130 <WIL> A; Cross-references: GB:K01084 R; Mercier, J.C.; Grossclaude, F.; Ribadeau-Dumas, B. Eur. J. Biochem. 23, 41-51, 1971 A; Title: Structure primaire de la caseine alpha-s1-bovine. Sequence complete. A; Reference number: A91188; MUID:72063417; PMID:4331376

A; Contents: B variant A; Accession: A91188

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1 QMEAEXIXXXEEIVPNXVEQK 21
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                                       Biokhimiia 51, 1402-1409, 1986
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-206 <MER>
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 6
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                                                                                                                                                                                                                                                                                                A.Molecule type: protein
A.Residues: 16-44,'Q',46-67,'T',69-214 <GRO>
A.Note: the D variant has a phosphorylated Thr at position 68
R.Grosclaude, F.F. Mahe, M.F.; Mercier, J.C.; Ribadeau-Dumas, B.
FEBS Lett. 11, 109-112, 1970
A.Title: Localisation, dans la partie NH-2-terminale de la caseine alpha-s1 bovine, d'un
A; Molecule type: protein
A; Residues: 16-44,'0',46-214 <MER>
A; Note: the sequences of residues 85-99 and of 125-140 are similar, having 10 identities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Molecule type: protein
A.Residues: 23-28,42-44,'Q',46-49 <GR2>
A.Residues: 23-28,42-44,'Q',46-49 <GR2>
A.Note: the sequence of the A variant lacks residues 29-41 of the B variant
R.Neuteboom, B.; Giuffrida, M.G.; Conti, A.
FEBS Lett. 305, 189-191, 1992
A.Title: Isolation of a new ligand-carrying casein fragment from bovine mammary gland mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 39-55 < NEU>
K; Grosclaude, F; Mercher, J.C.; Ribadeau-Dumas, B.
C. R. Acad. Sci. Hebd. Scances Acad. Sci. D 268, 3133-3136, 1969
A; Title: Sur la localisation, dans la sequence COOH-terminale de la caseine alpha-s1 bov
A; Reference number: A90738; MUID:69257961; PMID:4979278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Mocesabon: A90738
A; Mocesabon: A90738
A; Mocesabon: A90738
A; Mocesule type: protein
A; Residues: 205-206, 'G', '208-214 <GR3>
R; Grosclaude, F.; Mercler, J.C.; Ribadeau-Dumas, B.
C. R. Acad. Sci. D Sci. Nat. 271, 563, 1970
A; Reference number: A90740
A; Contents: annotation; erratum; C variant, revision
B; Exterkate, Pa.A.; Alting, A.C.; Slangen, C.J.
A; Title: Specificity of two genetically related cell-envelope proteinases of Lactococcus
A; Reference number: 513300; MUID:9113130; PMID:1899185
A; Contents: annotation; Cleavage by Lactococcus lactis subsp. cremoris cell-envelope profession. Biol. Chem. 48, 1663-1667, 1984
A; Ridgao, M; Maki, M; Sasaki, R; Chiba, R.
A; Title: Isolation and Sequence analysis of bovine alpha-s1-casein cDNA clone.
                                                                                                   Rigrosclaude, F.; Mahe, M.F.; Mercier, J.C.; Ribadeau-Dumas, B.
Eur. J. Biochem. 26, 328-337, 1972
A;Title: Caracterisation des variants genetiques des caseines alpha-S1 et beta bovines.
A;Reference number: A91192; MUID:72214259; PMID:5064450
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R;Kiarshullte, D.R.; Zakhar'ev, V.M.; Gordetskii, S.I.
Dokl. Akad. Nauk SSSR 280, 1433-1437, 1985
A;Title: [Nucleotide sequence of the 3'-nontranslated region of the mRNA of alpha S1-cas A;Reference number: 145852; MUID:85178933; PMID:3838718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 185-202 <MAK>
A;Cross-references: GB:D00412; NID:g217532; PIDN:BAA00313.1; PID:g217533
R;GorodetsKii, S.I.; Zakhar'ev, V.M.; Kyarshulite, D.R.; Kapelinskaya, T.V.; Skryabin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: translated from GB/EMBL/DDBJ
A;Molecule translated from GB/EMBL/DDBJ
A;Molecule translated from GB/EMBL/DDBJ
A;Residues: 122-202, 'L', 204-214 <KIA>
A;Cross-references: GB:M38658; NID:g162649; PIDN:AAA62707.1; PID:g162650
B;Maki, M.; Nagao, M.; Hirose, M.; Chiba, H.
Agric: Biol. Chem. 47, 441-444, 1983
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A;Molecule type: mRNA
A;Residues: 1-214 <NAG>
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A; Accession: A91274
                                                                                                                                                                                                                                                                       A; Accession: A91192
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C; Keywords: mammary gland; milk; phosphoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-214/Product: alpha-s1-casein #status predicted <MAT>
F;16-31,63,79,81,82,83,90,130/Binding site: phosphate (Ser) (covalent) #status experimen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: A25669
R; Mercier, J.C.; Gaye, P.; Soulier, S.; Hue-Delahaie, D.; Vilotte, J.L.
Biochimie 67, 959-971, 1985
A; Title: Construction and identification of recombinant plasmids carrying cDNAs codin
                                                                                                                                                                                                                                                                                                                                                                 A:Introns: 17/3; 28/3; 41/3; 49/3; 57/3; 65/3; 73/3; 84/3; 92/3; 110/3; 124/3; 132/3
C:Superfamily: alpha-s1-casein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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A;Description: Occurence of a LINE element in the 3' UTR of an allelic form of the
A;Reference number: S34262
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A;Title: Cloning and nucleotide sequence of cDNA for bovine alpha-S1-casein. A;Reference number: 145872
A;Accession: 145872
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C.Superfamily: alpha-s1-casein
C.Superfamily: alpha-s1-casein
C.Superfamily: alpha-s1-casein
F.1-15/Domain: signal sequence #status predicted <SIG>
F.16-206/Product: alpha-s1-casein #status predicted <KAl>
F.105-111/Region: opioid-like peptide sequence
F.79,80,81,82,83/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha-s1-casein precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 06-Jan 1995 #sequence_revision 06-Jan-1995 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                A)Status: translated from GB/EMBL/DDBJ
A)Molecule type: mRNA
A)Residues: 1-41,'L',43-142,'D',144-210,'IS',213-214 <G02>
A)Cross-references: GB:MA38641; NID:g1662793; PIDN:AAA30429.1; PID:g162794
C;Comment: The B variant sequence is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross references: GB:X03237; NID:g1247; PIDN:CAA26982.1; PID:g1248 A;Note: the authors translated the codon TCT for residue 27 as Asp C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.0%; Score 78; DB 1; Length 214; 76.2%; Pred. No. 1.5e-07; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.7%; Score 57; DB 1; Length 206
57.1%; Pred. No. 0.0018;
iive 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A25069; MUID:86104473; PMID:3002501
A; Accession: A25069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: S34262 .
R; Jansa, M.; Leroux, C.; Sanchez, A.; Martin, P.
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Gaps

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A; Molecule type: DNA
A; Residues: 1-215 cJOL>
A; Cross-references: GB:M77195
R; Devinoy, E.; Schaerer, E.; Jolivet, G.; Fontaine, M.L.; Kraehenbuhl, J.P.; Houdebir
Nucleic Acids Res. 16, 11813, 1988
A; Title: Sequence of the rabbit alpha(S1)-casein cDNA.
A; Reference number: S02042; MUID:89098329; PMID:3211752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Introns: 17/3; 28/3; 35/3; 49/3; 57/3; 65/3; 79/3; 87/3; 95/3; 105/3; 113/3; 128/3; 6;Superfamily: alpha-sl-casein
C;Superfamily: alphosphoprotein
C;Keywords: milk; phosphoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;1-15/Pomain: algnal sequence #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-814 <WIL>
A; Cross-references: EMBL:292803; PIDN:CAB07245.1; GSPDB:GN00021; CESP:K01G5.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Caenorhabditis elegans
C;Decies: Caenorhabditis elegans
C;Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-Sep-2000
C;Accession: T23200
R;Wall, M.
                                                                                                                                                                                                                                                                                                                                                                                                   arginasi-casein precursor - rabbit domestic rabbit)

C.Species: Oryctolagus cuniculus (domestic rabbit)

C.Species: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 13-Aug-1999

C.Accession: JC1133; S02042

R.Johivet, G.; Devinoy, E. Fontaine, M.L.; Houdebine, L.M.

R.Johivet, G.; Devinoy, E. Fontaine, M.L.; Houdebine, L.M.

A.Fitle: Structure of the gene encoding rabbit alpha-s1-casein.

A.Reference number: JC1133; MUID:92241677; PMID:1572547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S02042
A; Molecule type: mRNA
A; Residues: 1-215 < DEV>
A; Cross references: EMBL: X13042; NID:g1513; PIDN: CAA31448.1; PID:g1514
A; Cross references: A; Cenetics: A; Genetics: A; Cross references: A; Cros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 3
A;Introns: 7/1; 52/2; 78/2; 112/1; 156/2; 216/3; 702/3; 753/2
C;Superfamily: Caenorhabditis elegans hypothetical protein K01G5.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.0%; Score 44; DB 2; Length 814;
42.1%; Pred. No. 2.8;
tive 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 2; Length 215; Pred. No. 0.63;
65.1%; Score 54; DB 2; Length 214; 52.4%; Pred. No. 0.0071; tive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, March 1997
A;Reference number: 219706
A;Accession: T23200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 ETEASISSSEEIVPSSTKOK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: clone K01G5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QMEAEXIXXXEEIVPNXVEQK 21
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                                                                                                                                                                  1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                     74 QMKAGSSSSEEIVPNSAQQK 94
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                                                                                                  11; Conservative
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Best Local Similarity
Local 9; Conservat
                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
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C; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; Species: 29-dan-1993 #sequence_revision 29-Jan-1993 #text_change 13-Aug-1999
C; Accession: S07130; S27101
R; Hall, L.; Laird, J.E.; Craig, R.K.
Biochem. J. 222, 561-770, 1984
A; Title: Nuclectide sequence determination of guinea-pig casein B mRNA reveals homology
A; Reference number: S07130; MUID:85022410; PMID:6548375
A; Accession: S07130; MUID:85022410; PMID:6548375
A; Accession: S07130
A; Molecule type: mRNA
A; Residues: 1-198 AHALl>
A; Cross-references: EMBL:X00938; NID:g49574; PIDN:CAA25452.1; PID:g757817
A; Accession: S27101
A; Molecule type: Protein
A; Residues: 16-31 AHAL2>
C; Superfamily: alpha-s1-casein
C; Superfamily: phosphoprotein
C; Keywords: milk: phosphoprotein
C; Keywords: milk: phosphoprotein
F; 1-15/Domain: signal sequence #status predicted <SIG>F; 16-198/Product: casein B #status experimental <MAT>
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A, Residues: 1-214 <LE2>
A, Cross-references: EMBL:X59836; NID:9953; PIDN:CAA42496.1; PID:9954
A, Cross-references: EMBL:X59836; NID:9953; PIDN:CAA42496.1; PID:9954
R;Brignon, G.; Mahe, M.F.; Grosclaude, F.; Ribadeau-Dumas, B.
Protein Seq. Data Anal. 2, 181-188, 1989
A,Title: Sequence of caprine alpha(s1)-casein and characterization of those of its genet
A, Reference number: S06102; MUID:89331508; PMID:2755948
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J. Biol. Chem. 267, 1977, 1992
J. Biol. Chem. 267, 1977, 1992
A;Title: Mutations away from splice site recognition sequences might cis-modulate altern A;Reference number: A42158; MUID:92210588; PMID:1372900
A;Reference number: A42158; MUID:92210588; PMID:1372900
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C;Date: 30-Sep-1991 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
C;Accession: I46167; S06102; S15489
                                                                                                              A;Cross-references: EMBL:X72221; NID:g311942; PIDN:CAA51022.1; PID:g311943
C;Superfamily: alpha-s1-casein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                 Length 214;
                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                     Score 57; DB 2;
Pred. No. 0.0018;
1; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OMEAEXIXXXEEIVPNXVEOK 21
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                                                                                                                                                                                                                                                                                                                                                                                               1 OMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                          68.7%;
57.1%;
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                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                  A; Residues: 1-214 <JAN>
                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S06102
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C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

C; Accession: C70205

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alpha-casein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 13-Aug-1999
C;Accession: A56060
R;Grusby, M.J.; Mitchell, S.C.; Nabavi, N.; Glimcher, L.H.
Proc. Natl. Acad. Sci. U.S.A. 87, 6897-6901, 1990
A;Title: Casein expression in cytotoxic T lymphocytes.
A;Accession: A56060
A;Stetus: preliminary
A;Molecule type: mRNA
A;Kesidues: 1-313 GGRJ
A;Cross-references: GB:M36780; NID:9191574; PIDN:AA837142.1; PID:9191575
C;Superfamily: alpha-s1-casein
C;Keywords: phosphoprotein
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0
                                                                                                                                                                                                                                                                                                                                 A:Wolecule type: DNA
A:Residues: 1-93 (WIL>
A:Cross-references: EMBL:Z48543; PIDN:CAA88434.1; GSPDB:GN00020; CESP:C18D1.3
A:Experimental source: clone C18D1
R:Li, C.; Nelson, L.S.; Memmott, J.M.
Submitted to the EMBL Data Library, January 1998
A;Reference number: Z22162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                   C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C.Accession: T19384; T42411
R.Berks, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.4%; Score 41; DB 2; Length 93; 33.3%; Pred. No. 0.94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                             A;Accession: T19384
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: AF042390; PIDN: AAC08941.1
                                                                                                                                              FMRFamide-like peptide 4 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                      Submitted to the EMBL Data Library, March 1995
A; Reference number: Z19117
                                           190 OSEKEWLNVFOEVIPNLVE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 EQEEKNIASPDELIPEIVEQO 57
  1 QMEAEXIXXXEEIVPNXVE 19
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Best Local Similarity 33.30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Gene: flp-4; C18D1.3
A, Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-93 <LIC>
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hypothetical protein BB0844 - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete)

RESULT 10

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R) Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; W son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; W nature 390, S0. S080-S86, 1997

B) Whithous: Smith, H.O.; Venter, J.C.

A; Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A; Reference number: A70100; MuID:98065943; PMID:9403685

A; Actaus: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Cross-references: GB.AB001183; GB:AB00783; NID:92688786; PIDN:AAG67199.1; PID:9268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Arabidopsis thaliana (mouse-ear cress)
CiDate: 16-Uul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
CiAccession: T10627
Ribevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lem submitted to the Protein Sequence Database, June 1999
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A; Introns: 145/1; 171/2; 196/1; 242/3; 269/3; 298/3; 347/3; 374/3; 414/3; 442/3; 505/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: T20355
Accession: T20355
R;Wilkinson, J.
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A.Introns: 21/3; 160/1; 238/3; 328/3; 391/3
C.Superfamily: Caenorhabditis elegans hypothetical protein D2030.3
                                                                                                                                                                                                                                                                                                                                            47.0%; Score 39; DB 2; Length 323;
40.0%; Pred. No. 9.3;
Live 4; Mismatches 8; Indels
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A;Residues: 1-1396 <BEV>
A;Cross-references: EMBL:AL080282; GSPDB:GN00062; ATSP:T13K14.10
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52.6%; Pred. No. 15;
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Best Local Similarity 52.68
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hypothetical protein YOL109w - yeast (Saccharomyces cerevisiae)

N.Alternate names: hypothetical protein 00738

S.Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 06-Feb-1998
C;Accession: S66805
A;Recence number: S66791
A;Recence number: S66791
A;Recence number: S66805
A;Rocsidues: 1-113 CDNA
A;Restimental Source: strain S288C
C;Genetics:
C;Genetics:
A;Cross-references: SGD:S0005469; MIPS:YOL109w
A;Cross-references: SGD:S0005469; MIPS:YOL109w
A;Cross-references: SGD:S0005469; MIPS:YOL109w
A;Map position: 15L
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circumsporozoite protein - Plasmodium gallinaceum
c;Species: Plasmodium gallinaceum
c;Species: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 21-Jul-2000
c;Accession: JC6164
R;McCuchan, T.F; Kissinger, J.C.; Touray, M.G.; Rogers, M.J.; Li, J.; Sullivan, M.; Br Proc. Natl. Acad. Sci. U.S.A. 93, 11889-11894, 1996
A;Title: Comparison of circumsporozoite proteins from avian and mammalian malarias: Biol A;Reference number: JC6164; MUID: 97030292; PMID: 8876233
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A;Molecule type: DNA
A;Residues: 1-388 <MCC>
A;Residues: 1-388 <MCC>
A;Cross_references: GB:U65959; NID:g1663571; PIDN:AAC47344.1; PID:g1663572
C;Comment: This protein has an important immunogenicity.
C;Genetics:
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Best Local Similarity 72.7%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.8%; Score 38; DB 2; Length 113;
42.1%; Pred. No. 4.5;
tive 4; Mismatches 7; Indels
                                                       Query Match
Best Local Similarity 38.1%; Pred. No. 4%;
Matches 8; Conservative 5; Mismatches 8; Indels
131/3; 1139/3; 1163/3; 1194/3; 1226/3; 1259/3; 1290/3; 1344/3
                                                                                                                                                                                                                                                        913 KVEAEALLASEKLVPIAVLNK 933
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Matches 8; Conservative
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C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 24-Sep-1998
C;Accession: A37351
R;Paine-Saunders, S., Fristrom, D.; Fristrom, J.W.
Dev. Biol. 140, 337-351, 1990
A;Title: The Drosophila IMP-E2 gene encodes an apically secreted protein expressed du A;Title: The Drosophila IMP-E2 gene encodes an apically secreted protein expressed du A;Reference number: A37351; MUID:90323384; PMID:2115480
A;Reference number: A37351; MUID:90323384; PMID:2115480
A;Reference number: A37351; MUID:90323384; PMID:2115480
A;Reference number: A37351; MUID:9705411; PID:9157752
A;Cross-references: GB:M55099; NID:9705411; PID:9157752
C;Gene: FlyBase:FBgn0001254
A;Cross-references: FlyBase:FBgn0001254
A;Cross-references: FlyBase:FBgn0001254
Query Match
Best Local Similarity 42.1%; Pred: No. 22;
A;Cross-references: B; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
Matches 8; Conservative 3; Mismatches
Oy 3 EAEXIXXXEIVPNXVEOR 21
Db 171 EFTVVVPAEELSPNPVEOR 189
Search completed: February 11, 2003, 18:21:12
Job time: 20.4021 secs
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February 11, 2003, 18:07:35; Search time 9.30928 Seconds (without alignments) 93.563 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ATPO_RAPSA DNLI_PYRKO TKT_BACHD DPOZ_AERPE YFC4_YEAST VGR1_MOUSE VGR1_RAT Z335_HUMAN GL13_XENLA ARAC_HUMAN MAPA_RAT
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ALIGNMENTS	RESULT 1 CASI_BOVIN STANDARD; PRT; 214 AA. ID CASI_BOVIN STANDARD; PRT; 214 AA. CASI_BOVIN STANDARD; PRT; 214 AA. DT 21-UUL-1986 (Rel. 01, Created) DT 01-NOV-1990 (Rel. 16, Last sequence update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DE Alpha-SI casein precursor.	GN CSN1S1. S Bos taurus (Bovine). C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; C Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; OC Bovidae; Bovinae; Bos. OX NCBI_TaxID=9913;		RN [2] RN SEQUENCE FROM N.A. RA Nagao M., Maki M., Sasaki R., Chiba R.; RT "Isolation and sequence analysis of bovine alpha-Sl-casein cDNA RT Clone."; RL Agric. Biol. Chem. 48:1663-1667(1984).				RP SEQUENCE OF 122-214 FROM N.A. RP SEQUENCE OF 122-214 FROM N.A. RX MEDLINE=85178933; PubMed=3838718; RA Kiarshulite D.R., Zakhar'ev V.M., Gorodetskii S.I.; RT "Nuclectide sequence of the 3'-nontranslated region of the mRNA of RT "Nuclectide sequence of the 3'-nontranslated region of the mRNA of RT alpha S1-casein in cows."; RT Dokl. Akad. Nauk SSSR 280:1433-1437(1985). RN [7] RN [7] RP SEQUENCE OF 164-214 FROM N.A. RR MEDLINE=94154154; PubMed=1343827;
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us-09-380-738a-1.rsp

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SEQUENCE OF 23-49 (VARIANT A).
Grosclaude F., Mahe M.-F., Mercier J.-C., Ribadeau-Dumas B.;
"Localization in the N-terminal part of bovine casein alpha-sl of a 13 amino-acid deletion that differentiates variant A from variants B
Chen R., Wang B., Zhang Y., Liu W., Zhang J., Lao W.; "Cloning, mapping, and sequencing of 3' and its flanking region of bovine alpha-sl casein gene."; Chin. J. Biotechnol. 8:235-245(1992).
                                                                      MEDLINE-72063417; PubMed-4331776; Mercier J.-C., Grosclaude F., Ribadeau-Dumas B.; Primary structure of bovine alpha-s1 casein. Complete sequence."; Cur. J. Biochem. 23:41-51(1971).
                                                                                                                                                                                                                                                                                                                                                                                                  Grosclaude F., Mercier J.-C., Ribadeau-Dumas B., "On the localization in the C-terminal Sequence of bovine casein alpha-s1 of a Glu/Gly substitution that differentiates the genetic variants B and C.";
                                                                                                                                                                                                                                        Grosclaude F., Mahe M.-F., Mercier J.-C., Ribadeau-Dumas B.;
"Characterization of genetic variants of alpha-Sl and beta bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISION (VARIANT C).
Grosclaude F., Mercier J.-C., Ribadeau-Dumas B.;
C. R. Acad. Sci., D, Sci. Nat. 271:563-563(1970).
-i- FUNCTION: IMPORTANT ROLE IN THE CAPACITY OF MILK TO TRANSPORT
                                                                                                                               REVISIONS TO 74 AND 92-93 (VARIANTS A; B; C AND D).
MEDLINE=74082545; PubMed-4797901;
Mercier J.-C., Grosclaude F., Ribadeau-Dumas B.;
"Primary structure of alpha casein and of bovine beta casein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R. Acad. Sci., D, Sci. Nat. 268:3133-3136(1970).
                                                                                                                                                                                              J. Biochem. 40:323-323(1973).
                                                                                                                                                                                                                                                                                J. Biochem. 26:328-337(1972).
                                                                                                                                                                                                                    SEQUENCE (VARIANT D).
MEDLINE=72214259; Pubmed=5064450;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 205-214 (VARIANT C).
                                                            SEQUENCE OF 16-214 (VARIANT B)
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                                                                                                                                                                                 Correction.
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EMBL; X00564; CAB57792.1; -. EMBL; M33123; AAA30428.1; -. EMBL, X59856; CAA42516.1; EMBL, K01084; AAA30478.1; EMBL, EMBL, SAA530471.1; EMBL, S72388; AAD14099.1; --EMBL; M38641; AAA30429.1; -. A23071. S02202. S22575. A03106; KABOSB. PIR; A03106; PIR; A23071; PIR; S02202; PIR; S22575; PIR; S02675; PIR; S02575; PIR;

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                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mercier J.C., Gaye P., Soulier S., Hue-Delahaie D., Vilotte J.-L., "Construction and identification of recombinant plasmids carrying beta-lactoglobulin. Nucleotide sequence of alpha Sl-, alpha Sl-, beta-, kappa-casein and Blochimie 67:959-971(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                  PHOSPHORYLATION (IN VARIANT D). PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                           Length 214;
                                                                                                                                                                                                                                                                                                                                                  Pred. No. 4.8e-07; insmatches 5; Indels
                                                                                                                                                                                                                   A -> T (IN VARIANT D).
P -> L (IN REF. 3).
E -> Q (IN REF. 4 AND 11).
H -> D (IN REF. 5).
H -> D (IN REF. 5).
S -> L (IN REF. 6).
                                                                                                                                                                                                                                                                                                              24529 MW; F066B5C8AE55828B CRC64;
                                                                                                                                                                                                           (IN VARIANT A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALCIUM PHOSPHATE.
-- SUBCELLULAR LOCATION: EXTRACELLULAR.
-- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-- SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
                                                                                                                                                                                                                                                                                                       (IN REF
                                                                                                                                                                                                                                                                                                                                         Score 78; DB 1;
                                                                          PHOSPHORYLATION PHOSPHORYLATION
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                                                                ALPHA-S1 CASEIN
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01-NOV-1997 (Rel. 35, Last annotation update)
           Pfam; PF00363; caseins; 2.
PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
Milk; Phosphorylation; Signal; Repeat.
                                                                                                                                                                                                                                                                             H -> D (II
S -> L (II
MP -> IS
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MEDLINE=86104473; PubMed=3002501;
                                                                                                                                                                                                                                                                                                                                                            0;
 InterPro; IPR001588; Casein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1987 (Rel. 05, Created)
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P04653;
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Two of the three genetic variants of goat alpha s1-casein which are synthesized at a reduced level have an internal deletion possibly due to altered RNA splicing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perez M.J., Leroux C., Bonastre A.S., Martin P.; "Occurrence of a LINE sequence in the 3' UTR of the goat alpha sl-casein E-encoding allele associated with reduced protein synthesis
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mutations away from splice site recognition sequences might cis-
modulate alternative splicing of goat alpha sl-casein transcripts.
Structural organization of the relevant gene.";
                                                                                                                                                                                                                                                                                                                                                                Capra hircus (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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01-0CT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Alpha-S1 casein precursor (Alpha-S1-CN) (Variants A, B, C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brignon G., Mahe M.-F., Ribadeau-Dumas B., Mercler J.-C., Grosclaude F.;
                                                                                                                                                                 Length 206;
                                                                                        PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
                                                                                 OPIOID-LIKE PEPTIDE SEQUENCE.
                                                                                                                       PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
26955ED115A5852B CRC64;
                                                                                                                                                                     DB 1;
                                                                         ALPHA-S1 CASEIN.
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1; Mismatches
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                                  Intering Proposition State Press 1.
PROSTITE: PS00306; CASEIN.ALPHA_BETA: 1.
Milk: Phosphorylation; Signal.
1 15
                                                                                                                                                                     Score 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 267:6147-6157(1992).
                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE=95011611; PubMed=7926797;
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MEDLINE-92210588; PubMed=1372900;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (VARIANT E).
                                                                                                                                      83 PI
23303 MW;
                                                                                                                                                                                                                        1 QMEAEXIXXXEEIVPNXVEQK 21
                PIR; A25069; KASHS1.
InterPro; IPR001588; Casein.
       EMBL; X03237; CAA26982.1; -.
                                                                                                                                                                     68.78;
                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Caprinae; Capra.
                                                                                                                                                                                        Conservative
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es 12; Conserv
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P18626;
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Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
Protein Seq. Data Anal. 2:181-188(1989).
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                                                                                                           -:- SUBCELLULAR LOCATION: EXTRACELLULAR.
-:- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-:- MISCELLANEOUS: THE SEQUENCE SHOWN IS VARIANT FORM B.
-:- SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
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57.1%; Pred. No. 0.003;
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Last annotation update)
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                                                                                           CALCIUM PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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P04656;
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MEDLINE=89098339; PubMed=3211752;
Bouldhoy E., Schaerer E., Jolivet G., Fontaine M.L., Kraehenbuhl J.P.,
Houdebine L.M.;
"Sequence of the rabbit alpha S1-casein cDNA.";
Nucleic Acids Res. 16:11813-11813(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
  conservation of the non-coding regions of the mRNA.";
Biochem. J. 222:561-570(1984).
-!- FUNCTION: IMPORTANT ROLE IN THE CAPACITY OF MILK TO TRANSPORT
CALCIUM PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Pred. No. 0.0064;
1; Mismatches 9; Indels
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PHOSPHORYLATION (POTENTIAL)
PHOSPHORYLATION (POTENTIAL).
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BEDLINE-92241677; PubMed=1572547;
Jolivez (G., Devinoy E., Fontaine M.L., Houdebine L.M.;
"Structure of the gene encoding rabbit alpha s1-casein.";
Gene 113:257-262(1992).
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                                                                                                    -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-!- SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
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01-FEB-1994 (Rel. 28, Last annotation update)
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52.4%;
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P09115:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rhabditidae; Peloderinae: Caenorhabditis
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MEDLINE-97540342; PubMed=9110175;
Clines G.A., Ashley J.A., Shah S., Lovett M.;
"The structure of the human multiple exostoses 2 gene and characterization of homologs in mouse and Caenorhabditis elegans.";
Genome Res. 7:359-367(1997).
-!- FUNCTION: IMPORTANT ROLE IN THE CAPACITY OF MILK TO TRANSPORT
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40737A027636B255 CRC64;
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                                                                          -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
-1- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-1- SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
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3; Mismatches
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Plan; PF00363; caseins; 1.
PROSITE; PS00306; CASEIN ALPHA_BETA; 1.
Milk; Phosphorylation; Signal.
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25528 MW;
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                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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               FUNCTION: Probable alphal, 4.N-acetylglucosaminyltransferase required for the biosynthesis of heparan-sulfate (By similarity). SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
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N-LINKED (GLCNAC...) (POTENTIAL).
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"Casein expression in cytotoxic T lymphocytes.";
Proc. Natl. Acad. Sci. U.S.A. 87:6897-6901(1990).
-1- FUNCTION: IMPORTANT ROLE IN THE CAPACITY OF MILK TO TRANSPORT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                              reticulum (By similarity).
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                                                                                                                                                                                                                                                                                                               Transferase; Glycosyltransferase; Endoplasmic reticulum;
      Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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-:- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-:- SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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4; Mismatches
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MEDLINE=90370891; PubMed=2395885;
                                                                                                                                                                                                                                                                                        InterPro, IPR004263; Exostosin.
Pfam; PF03016; Exostosin; 1.
                                                                                                                                                                                                                            EMBL; U94835; AAC47510.1; -. EMBL; AB077851; BAB83878.1; -. EMBL; Z92803; CAB07245.1; -. Wormpep; K0165.6; CE16196.
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P19228;
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the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clarke A.K., Schelin J.; "The cyanobacterium Synechococcus sp. strain PCC 7942.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
CATALYTIC ACTIVITY: Hydrolysis of proteins to small peptides in
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
17-JUL-1998 (Rel. 41, Last annotation update)
17-JUL-1998 (Rel. 41, Last annotation update)
18-JUL-1998 (Rel. 41, Last sequence update)
18-JUL-1998 (Rel. 36, Last se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Bacteria: Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.0%; Score 39; DB 1; Length 313; 63.6%; Pred. No. 7.6; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
15 x 6 AA TANDEM REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                         program, PF0033; cascins; 1.
PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
Milk; phosphorylation; Repeat; Signal.
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                                                                                                                                                                                                                                                                                               PIR; A36060; A36060.
MGD; MGI:88540; Csna.
InterPro; IPR001588; Casein.
                                                                                                                                                                                                                                                                  EMBL; M36780; AAA37142.1; -.
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the presence of ATP and magnesium. Alpha-casein is the usual test substrate. In the absence of ATP, only oligopeptides shorter than five residues are cleaved (such as succinyl-Leu-Tyr-|-NHMEC; and Leu-Tyr-Leu-|-Tyr-Trp- in which the cleavage of the -Tyr-|-Leu-SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRIN-Berkeley;
MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paine-Saunders S., Fristrom D., Fristrom J.W., "The Drosophila IMP-E2 gene encodes an apically secreted protein expressed during imaginal disc morphogenesis.", Dev. Biol. 140:337-351(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
', 865EA0FC3F7600F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00382; CLP_PROTEASE_HIS; 1.
PROSITE; PS00381; CLP_PROTEASE_SER; 1.
Hydrolase; Serine protease; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMP2_DROME STANDARD; PRT; 466 AA. P29681; Q9VZN9; Clasted) Ol-APR-1993 (Rel. 25, Created) Ol-APR-1993 (Rel. 25, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 20-hydroxyecdysone protein precursor (20-HE). IMPE2 OR IMP-E2 OR CG1934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 444-454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.8%; Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001907; CLP_protease.
Pfam; PF00574; CLP_protease; 1.
PRINTS; PR00127; CLPPROTEASEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90323384; PubMed=2115480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 AA; 25986 MW;
                                                                                                                                                                                                                                                                                EMBL; U92039; AAB68677.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 OMEAEXIXXXEEIVPNXVEQ 20
                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGR00493; clpP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 OPOIGAIAGSQAIVPTVVEQ 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.08;
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                                                                                                                                                                                                                                                                                                                      MEROPS; S14.001
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SEQUENCE
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RA BOTKOVA D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.W., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,
RA Cosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Jalain M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Mernandez J.R., Houck J.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G. Milshina N.V., Mobarry C., Morris J., Mocherson D.L.,
RA Merkulov G. Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R. D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Stropg R., Sun E.,
RA Spier B.C., Siden-Kiamos I., Simpson M., Stropg R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Walliams S.M., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Walliams S.M., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.W., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Zheng C. P., Turner R. S., Chong S., Zho O., Zheng C., Sheng C., Shong G., Zhao O., Zheng S., Zhong O., Zheng C., Shong W., Zhou W., Zhou S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.D., Scibbe R., Shu B., Shu B This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). INDUCES MORPHOGENESIS OF INAGINAL DISKS, AND MAY PARTICIPATE IN DULTIMOLECULAR AGGREGATES.

SUBCELLUAR LOCATION: SECRETED FROM THE APICAL CELL SURFACE. DEVELOPMENTAL STAGE: PRODUCED DURING MID EMBRYOGENESIS, AND MAGINAL DISK MORPHOGENESIS.

DOMAIN: THE REGIONS 203-253, 256-333 AND 335-377 ARE THOUGHT TO CONTAIN EITHER ALPHA HELICAL OR BETA PLEATED SHEET MOTIFS. 1 (APPROXIMATE).
2 (APPROXIMATE).
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11 20-HYDROXYECDYSONE PROTEIN. 16 X REPEATS. POTENTIAL. .; AE003478; AAF47780.1; -A37351; A37351. ase; FBgn0001254; ImpE2. EMBL; M55099; AAA63632.1; -. Signal; Glycoprotein; Repeat. 49809 MW; 352 466 AA; FlyBase; CARBOHYD CARBOHYD SEQUENCE DOMAIN REPEAT REPEAT SIGNAL REPEAT CHAIN EMBL;

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synthetase.
                                                     NON_TER
SEQUENCE
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                                         VARSPLIC
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                            Makayama A., Odajima T., Murakami H., Mori N., Takahashi M.;
Nakayama A., Odajima T., Murakami H., Mori N., Takahashi M.;
Nakayama A., Odajima T., Murakami H., Mori N., Takahashi M.;
RT Transcripts in the microtubule-associated protein (MAP) 1A gene.";
Transcripts in the microtubule-associated protein (MAP) 1A gene.";
Elochim. Blophys. Acta 1218:260-266(2001)

L. FUNCTION: Structural protein involved in the filamentous cross-
I. FUNCTION: Structural protein involved in the filamentous cross-
I. SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
I. SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
I. SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
I. SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
I. SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
I. STORY SERVENCIONES: 2 isoforms; a long form (shown here) and a
Short form; are produced by alternative splicing.
I. ALTERNATIVE PRODUCTS: 2 isoforms; a lightly expressed in brain, and
I. ALTERNATIVE PRODUCTS: 2 isoforms lightly expressed in classer extent in other tissues including heart and muscole.
I. DOMAIN: THe basic region contraining the repeats may be responsible for the binding of MAPIA to microtubules.
I. PUN: Various serine residues may be phosphorylated by CAMP kinase
                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LÎS-RICH (BASIC).
11 X 3 AA APPROXIMATE REPEATS OF K-K-
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation; Alternative splicing.
                                                     ..
                         45.8%; Score 38; DB 1; Length 466; 42.1%; Pred. No. 17;
                                                     8; Indels
                                                                                                                                                                                       090YR66 0902H9; Q90ZIO; 090ZII; Corr-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) 16-0CT-2001 (Rel. 40, Last annotation update) Microtubule-associated protein IA (MAP IA) (Fragment) MAPIA OR MTAPI
                                                                                                                                                                                   PRT; 1021 AA.
                                              42.1%; Pred. M. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF182211; AAF06164.1; -... EMBL; AF182208; AAF06164.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF182213; AAF06164.1; JOINED. AF182211; AAF06163.1; AF182213; AAD55790.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF182212; AAD55789.1;
                                                                                                        | : ||: || ||:
171 EETVVVPAEELSPNPVEQE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity).
                                                                                        3 EAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mtap1.
                                         Query Match
Best Local Similarity 42.1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microtubules; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:97174;
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD;
                                                                                                                                                                  RESULT 10
                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andrews S., Langston Y., Stoneking T., Maupin R.;
Submitted (Jun'1998) to the EMBL/GenBank/DDBJ databases.
--- CATALYTIC ACTIVITY: ATP + 91ycine + tRNA(G1y) = AMP + diphosphate + g1ycy1-tRNA(G1y).
--- SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shiba K., Schimmel P., Motegi H., Noda T.; Induna giyothetase. Wide divergence of primary structure from bacterial counterpart and species-specific aminoacylation."; J. Biol. Chem. 269:30049-30055(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams J.H., Osvath S.R., Khong T.-F., Pearse M.J., Power D.A.; "Cloning, sequencing and bacterial expression of human glycine tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  P41250; 096971;
01-FEB-1995 (Rel. 31, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
01ycyl-tRNA synthetase (EC 6.1.1.14) (Glycine-tRNA ligase) (GlyRS).
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ge Q., Trieu E.P., Targoff I.N.; "Primary structure and functional expression of human glycyl-tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                 ;
0
                                                                                                                                               45.8%; Score 38; DB 1; Length 1021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                    8; Indels
                                                                                                  1021 AA; 113064 MW; 69F2700C6867DBBB CRC64;
                                               MISSING (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthetase, an autoantigen in myositis.";
J. Biol. Chem. 269:28790-28797(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                  739 AA.
                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Núcleic Acids Res. 23:1307-1310(1995).
                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95050687; PubMed=7961834;
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95273165; PubMed=7753621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=95050870; PubMed=7962006;
                                                                                                                                                                                                                                                                                                              807 LEQEQVEREKEVVPDFPEDK 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 3-739 FROM N.A.
                                                                                                                                                                                                                                                              2 MEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                            35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Eye, and Muscle;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                    7; Conservative
               675
765
224
1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
668
673
763
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Gaps

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Ouery Match
Best Local Similarity 63.68; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 3; Indels

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CHAIN 16 206 ALPHA-SI CASEIN. SEQUENCE 206 AA; 24148 MW; 58670C0B309A4456 CRC64;

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                                                                                                                                                                                                   Pfam: PF03129; HRNA-synt_2b; 1.
Pfam: PF03129; HRNA-synt_2b; 1.
PRINTS: PR01043; TRNASYNTHGLY.
TIGRRAMS; TIGR00389; G1yS_dimeric; 1.
PROSITE; PS50862; MATRNA_LIASE_LI; 1.
PROSITE; PS00762; WHEP_TRS; 1.
Aninoacyl-trnA synthetase; Protein biosynthesis; Ligase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Mammary gland;
MEDLINE-92367946; PubMed-1503265;
Alexander L.J., Beattie C.W.;
"The sequence of portine alpha s1-casein cDNA: evidence for protein variants generated by altered RNA splicing.";
Anim. Genet. 23:283-288(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                               44.6%; Score 37; DB 1; Length 739;
66.7%; Pred. No. 39;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                 530 530 M -> I (IN REF. 2).
739 AA; 83139 MW; 55DDD57119F438E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i - TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P39035;
01-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 AA.
                                                                                                                    InterPro; IPR002106; AAtRNA_ligaseII.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR000738; WHEP-TRS.
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR002315; tRNA-synt_2b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Extracellular.
EMBL; D30658; BAA06338.1; -
EMBL; U09510; AAA86443.1; ALT_INIT.
EMBL; BC007722; AAH07722.1; -
EMBL; BC007755; AAH07755.1; -
                                                     EMBL; U0958; AAA57001.1; ALT_INIT.
EMBL; AC004976; AAC71652.1; --
HSSP; P56206; 1ATI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                          Pfam; PF00458; WHEP-TRS; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X54973; CAA38717.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A45661; A45661.
InterPro; IPR001588; Casein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-S1 casein precursor.
                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                             HGNC:4162; GARS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       568 EEVVPNVIE 576
                                                                                                                                                                                                                                                                                                                                                                                                              11 EEIVPNXVE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
                                                                                                             MIM; 600287:
                                                                                                                                                                                                                                                                                                                 CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAS1_PIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;
The complete genome sequence of the lactic acid bacterium Lactococcus lactis structis IL1403.";
Genome Res. 11:731-753(2001).

FUNCTION: This protein is involved in the repair of mismatches in bush. It is possible that it carries out the mismatch recognition step. This protein has a weak APPase activity (By similarity).

SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria: Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSUCACES, MULCAL, T. TICREMAIS, STUCACES, MULCAL, MULCAL, MULCALLE, PSO0486; DNA_MISKATCH_REPAIR_2; 1.
DNA repair; ATP-binding; DNA-binding; Complete proteome.
NP_BIND 601 608 ATP (POTENTIAL).
SEQUENCE 840 AA; 94272 MW; 867EFE4F82616DC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                       Journal (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA mismatch repair protein muts.
MUTS OR HEXA OR LL2210.
                                                                                                                                                                                                                                                              840 AA
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40.0%; Pred. No. 66;
tive 3; Mismatches
                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=1L1403;
MEDLINE=21235186; PubMed=11337471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE006450; AAK06308.1; -
InterPro; IPR000432; MutS_C.
InterPro; IPR002863; MutS_N.
Pfam; PF01648; MutS_N.
Pfam; PF01624; MutS_N; 2.
ProDom; PD001263; MutS_C; 1.
                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 40.0 les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00534; MUTSac;
SMART; SM00533; MUTSd; 1
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11 EEIVPNXVEQK 21
                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     MUTS_LACLA
Q9CDK9;
                                                                                                                                                                                                    MUTS_LACLA
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                                                                                                                                                             RESULT 13
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                                                                                                                                                                                                                                                                                                                                            RX MEDLINE=21848401; PubMed=11859360; M. Lyne M., Lyne R., Stewart A., RA MEDLINE=21848401; PubMed=11859360; M. Lyne M., Lyne R., Stewart N., Hayles J., Basker S., Basham D., Bowan S., Sqourcos J., Peat N., Hayles J., Basker S., Basham D., Down D., Brown S., Chillingworth T., Churcher C.M., Broks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Connor R., Cornor R., Harlin N., Harris D., Hidalgo J., Hadgen G., Achtels S., Gobbe A., Hamilin N., Harris D., Hidalgo J., Hadgen G., Bachter S., McDonald S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A new member of the Sin3 family of corepressors is essential for cell viability and required for retroelement propagation in fission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: TO YEAST PAIRED AMPHIPATHIC HELIX PROTEIN (SIN3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dang V.D., Benedik M.J., Ekwall K., Choi J., Allshire R.C., Levin H.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1075 AA; 124848 MW; 1AD301DB4EB1AFFB CRC64;
                                                              16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
paired amphipathic helix protein pst2 (Sin3 homolog).
                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                      PRT; 1075 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ceil. Biol. 19:2351-2365(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z98559; CAB11171.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR003822; PAH. Pfam; PF02671; PAH; 3.
                                STANDARD;
                                                                                                                                                                        PST2 OR SPAC23C11.15.
                                                                                                                                                                                                                                                                          Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                          SCHPO
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                    PST2_SCHPO
RESULT 14
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STRUCTURE BY NMR OF 129-229.

STRUCTURE BY NMR OF 129-229.

STRUCTURE STRUCTURE STRUCTURE M.A., Christinger H.W., Wiesmann C., Champe M.A.,

Starovasanik M.A., Christinger H.W., Wiesmann C., Champe M.A.,

Starovasanik M.A., Christinger H.W., Wiesmann of Flt-1: Comparison
de Vos A.M., Stelton N.J.;

solution structure of the VEGF-binding domain of Flt-1: comparison
of its free and bound states.";
of its free and bound states.";
J. Mol. Biol. 293:531-544(1999).
J. Mol. Biol. 293:531-544(1999).

FUNCTION: Receptor for VEGF, VEGFB and PGF. Has a tyrosine-protein
kinase activity. The VEGF-kinase ligand/receptor signaling system
plays a key role in vascular development and regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kendall R.L., Thomas K.A.;
"Inhibition of vascular endothelial cell growth factor activity by an endogenously encoded soluble receptor.";
proc. Natl. Acad. Sci. U.S.A. 90:10705-10709(1993).
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MEDLINE-8730f538; PubMed=3040650;
Matsushime H., Yoshida M.C., Sasaki M., Shibuya M.;
Ma possible new member of tyrosine kinase family, human frt sequence, is highly conserved in vertebrates and located on human chromosome
                                                                                                                                                                    VGRI_HUMAN STANDARD, PRT; 1338 AA.

VGRI_HUMAN STANDARD, Created)
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last parnotation update)
Vascular endotbelial growth factor receptor 1 precursor (BC 2.7.1.112)
Vascular permeablility factor receptor) (Tyrosine-protein kinase receptor FLT) (FLt-1) (Tyrosine-protein kinase FRT) (Fms-like tyrosine kinase 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence and expression of a novel human receptor-type tyrosine kinase gene (flt) closely related to the fms family."; oncogene 5:519-524(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human), Craniata; Vertebrata; Buteleostomi; Homo sapiens (Humazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM SFLT1), AND SEQUENCE OF N-TERMINUS
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Yu Y., Whitney R.G., Sato J.D.;
Yu Y., whitney R.G., human VEGF receptor FLT1 (VEGFR-1).";
"Coding region for human VEGF receptor FLT1 (VEGFR-1).";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibuya M., Yamaguchi S., Yamane A., Ikeda T., Tojo A.,
Matsushime H., Sato M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 273:23410-23418(1998).
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MEDLINE=90221591; PubMed=2158038;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name and the property of the p
                                                                                                                                                                               -!- NATERNATIVE PRODUCTS: At least 2 isoforms; Fit1 (shown here) and SFIt1; are produced by alternative splicing.
-! TISSUE SPECIFICITY: Mostly in normal lung, but also in placenta, liver, kidney, heart and brain tissues. Specifically expressed in peripheral blood monocytes. It is not expressed in peripheral blood monocytes. It is not expressed in tunes. Isoform sFIt1 is strongly expressed in tune. SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
         Vascular permeability. Isoform SFlt1 may have an inhibitory role in anglogenesis.
                                                 -!- SUBUNȚT: Interacts in vitro with various phosphotyrosine-binding Proteins, including PLC-gammas, PTPN11, GRB2, CRK and NCK1.
                                                                                                                 tyrosine phosphate.
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
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IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 3.
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IG-LIKE C2-TYPE DOMAIN 6.
IG-LIKE C2-TYPE DOMAIN 7.
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ATP (BX SIMILARITY).
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EMBL; AF063657; AAC1649.1; --
EMBL; U01134; AAC50060.1; --
EMBL; D00133; BAA00080.1; --
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PDB; 1QSV; 10-NOV-99.
PDB; 1QSZ; 10-NOV-99.
Genew; HGNC:3763; FLFI.
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Search completed: February 11, 2003, 18:17:43 Job time : 11.3093 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	062823 bubalus bub 09ts03 ovis aries 09ts03 ovis aries 09ts48 ovis aries 08spr1 equus cabal 099m19 mus musculu 099m19 mus musculu 091ym mus musculu 051784 borrelia bu p90790 caenorhabdi 09suc7 arabidopsis 008455 saccharomyc 095k27 equus cabal 094675 plasmodium 08rwx2 arabidopsis
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ALIGNMENTS

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                                                                                                 Bubalus bubalis (Domestic water buffalo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                     Das P., Jain S., Garg L.C.;
Das P., Jain S., Garg L.C.;
CDNA cloning and sequencing of asl-casein in Bubalus bubalis.";
submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ005410; CAA06533.1;
TherPro: IPR001588; Casein.
Pfam; PF00365; sassins; 1.
PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
SEQUENCE 214 AA; 24327 MW; AD837A5170156423 CRC64;
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                                           01-AUG-1998 (TrEMBLrel. 07, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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NCBI_TaxID=89462;
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Matches 15; Conservative
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Ferranti P., Malorni A., Nitti G., Laezza P., Pizzano R., Chianese L.,
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                                                                                                                                                             Addeo F.; "Primary structure of ovine alpha sl-caseins: localization of phosphorylation sites and characterization of genetic variants A, C
                                                                                                                                                                                                                                                                                                                               Gaps
                                        Ovis aries (Sheep).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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1 Similarity 57.1%; Pred. No. 0.0054;
12; Conservative 1; Mismatches 8; Indels
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SEQUENCE 191 AA; 21739 MW; 37C50FE3A4829ABE CRC64;
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Pfam; PF00363; caseins: 1
enouteNCE 199 AA; 22751 MW; C8D75CB2283E9A5B CRC64;
01-MAY-2000 (TrEMBLrel. 13, Last Sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) Alpha S1-casein A short form.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Alpha SI-casein A long form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           199 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95325458; PubMed=7601973;
                                                                                                                                                                                                                  J. Dairy Res. 62:281-296(1995).
InterPro; IPR001588; Casein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Dairy Res. 62:281-296(1995).
InterPro; IPR001588; Casein.
                                                                                                                                                                                                                                                                                                                                        1 OMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                       1 OMEAEXIXXXEEIVPNXVEOK 21
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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0
                                                                                                                                                                                  54.2%; Score 45; DB 6; Length 212; 42.9%; Pred. No. 1.2;
                                                                     SECUENCE FROM N.A.
Lenasi T., Rogelj I., Dovc P.;
Equus caballus alpha-s1-casein (as1-CN) mRNA.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AV040862; AAK83668.1;
SEQUENCE 212 AA; 25305 MW; 578F72EA76E26E6E CRC64;
                                                                                                                                                                                                 Pred. No. 1.2;
2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.4%; Score 41; DB 5; Length 93; 33.3%; Pred. No. 3; B; Indels ive 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li C., Nelson L.S., Memmott J.M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; 248543; CAA68434.1; -
EMBL; AF042399; AA60841.1; -
WormPep; C18D1.3; CE01503.
Hypothetical protein.
SEQUENCE 93 AA: 10347 MW; DADC271BC6F34FF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Hypothetical 10.3 kDa protein Cl8D1.3 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berks M.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                    93 AA.
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01-JAN-1999 (TrEMBLrel. 09, Created)
01-JAN-1999 (TrEMBLrel. 09, Last com
                                                                                                                                                                                                                                                                                                                                               PRT;
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01-JUN-2001 (TrEMBLrel. 17, Last seq
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                                                                                                                                                                                                                                        1 QMEAEXIXXXEEIVPNXVEQK 21
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les 9; Conserv
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                        47.0%; Score 39; DB 11; Length 294; 63.6%; Pred. No. 23; Live 1; Mismatches 3; Indels
                                                                        47.0%; Score 39; DB 11; Length 292; 63.6%; Pred. No. 22; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted When-2001) to the EMBL/GenBank/DDBJ databases. Submitted DC06024; AAH06024.1; ...
InterPro; IPR001588; Casein.
Pfam; PF00363; caseins; 1.
PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
SEQUENCE 305 AA; 34797 MW; 04800330BA6C38BF CRC64;
                                                                                                                                                                                                                                                                                                                                               Submitted (MAX-2001) to the EMBL/GenBank/DDBJ databases. BMBL, BC008278; AAH08278.1; -. InterPro; IPR001588; Casein. Pfam: PF00363; caseins; 1. PR0315: Caseins; 1. PR051TE; PS003306; CASEIN_ALPHA_BETA; UNKNOWN_1. SEQUENCE 294 AA; 33244 MW; 02347DF26D50989A CRC64;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JAN-2001). AAH02101.1; InterPro; IPR001588; Casein. Fram: PF00363; caseins: 1. PR05ITE; PS00306; CASEIN_ALPHA_BETA; 1. SEQUENCE 292 AA: 32988 WW; AF3C9B7A4889BFE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to casein alpha.
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Best Local Similarity boccons
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                                                                           Query Match
Best Local Similarity 63.0°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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Best Local Similarity
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                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                  TISSUE=BREAST TUMOR;
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                                                                                                                                          || :|| |||
| 98 EEAIPNITEOK 108
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                                                                                                                          11 EEIVPNXVEOK 21
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01-OCT-2001
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SEQUENCE FROM N.A.

STRAIN-ATCC 35210 / B31;

MEDLINE-98665943; PubMed-9403685;

MEDLINE-98665943; PubMed-9403685;

MEDLINE-98665943; PubMed-9403685;

MELAHIGTA R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., Lathigra R., White O., Ketchum K.A., Dodson R.D., Richardson D., Hougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Hanson M., Peterson J., Kerlavage A.K., Quadembush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Van Vugt R., Watthey L., McDonald L., Artlach P., Bowman C., Gutton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C.;

"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
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EMBL; 273906; CAA98117.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.0%; Score 39; DB 16; Length 323; 40.0%; Pred. No. 25;
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Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 399:580-586(1997).

EMBL; AE001183; AAC67199.1; -
TIGR; BB0844; -
Hypothetical protein; Complete proteome.

SEQUENCE 323 AA; 37466 MW; 312C1E2EIER49F5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 20, Last annotation update)
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     1; Mismatches
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01-MAN-1998 (TrEMBLrel. 05, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
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                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                       Hypothetical protein BB0844.
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            7; Conservative
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nes 8; Conserv
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|92 EEAIPNITEOK 102
                                                          11 EEIVPNXVEOK 21
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SEQUENCE FROM N.A. Durand P., Hilger
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094675;
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                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces crevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

NCBI_TaxID=4032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W.,
Mayer K.F.X., Lemcke K., Schueller C.;
Sübmitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                             DB 5; Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.0%; Score 39; DB 10; Length 1396; 38.1%; Pred. No. 1e+02;
                                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                 EU Arabidopsis sequencing project;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
508 AA; 56589 MW; 812AC8891A578B64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL080282; CAB45880.1;
EMBL; AL161553; CAB79085.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1396 AA; 154174 MW; 113209E42E9DE4E3 CRC64;
                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 154.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Chromosome XV reading frame ORF YOL109W.
                                                                                                                                                       PRT; 1396 AA.
                       47.0%; Score 39; DB
52.6%; Pred. No. 39;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE, PS00137; SUBTILASE_HIS; 1. PROSITE; PS00138; SUBTILASE_SER; 1. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000209; Peptidase_S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00082; Peptidase_S8; 3. PRINTS; PR00723; SUBTILISIN.
                                                                                     432 EMETEDKEEEIVPVVVEKK 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          913 KVEAEALLASEKLVPIAVLNK 933
                                                                 3 EAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QMEAEXIXXXEEIVPNXVEQK 21
                              Best Local Similarity 52.6 Matches 10; Conservative
                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S08.090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                Q9SUC7
                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   008245
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                                                                                                                                     09SUC
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Milenkovic D., Martin P., Guerin G., Leroux C.;
"Horse specific pattern of alphaS1-casein RNA splicing and genomic characterization of the relevant locus.";
Submitted (AuG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY049939; AAL05435.1; -
InterPro: IPR001588; Casein.
PROSITE; PS00306; CASEIN_ALPHA_BETA; UNKNOWN_1.
SEQUENCE 208 AA; 24689 MW; OCC6C409489C589C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97030292; PubMed-8876233; McCutchan T.F., Kissinger J.C., Touray M.G., Rogers M.J., Li J., Sullivan M., Braga E.M., Krettli A.U., Miller L.H.; "Comparison of circumsporosoite proteins from avian and mammalian malarias: biological and phylogenetic implications."; EMBL; U65959; AAC47344.1; -.. 93:11889-11894(1996).
                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                      45.8%; Score 38; DB 3; Length 113;
42.1%; Pred. No. 14;
tive 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium gallinaceum.
Eukaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                 7; Indels
                                                                                      Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.8%; Score 38; DB 6; Length 208;
Durand P., Hilger F., Portetelle D., Vandenbol M.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Indels
                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last Sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              208 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 25;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 QOESSISSEEVVPINTERR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QMEAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                              ||| : |: : |||| 5
51 EAEQVKKEEQNIADGVEQK 69
                                                                                                                                                                                                                                                          3 EAEXIXXXEEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.3%;
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                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 33.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Circumsporozoite protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                     Local Similarity
nes 8; Conserv
                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9796;
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                                                                                                                                                                                      Query Match
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeguerice From N.A.

Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,

Yamada K., Banh J., Chan M.M., Chang C.S., Quach H.L.,

Dong J.M., Coldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,

Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

Kamiya A., Karlin-Neumann G., Kawai J., Xim C., Lam B., Lin J.,

Meyers M.C., Miranda M., Shinn P., Southwick A., Shinozaki K.,

Bakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,

Davis R.W., Ecker J.R., Theologis A.,

"Arabidopsis Full Length CDNA Clones."

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AV091048: AAM13869.1; -.
                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.8%; Score 38; DB 10; Length 504;
42.1%; Pred. No. 60;
tive 3; Mismatches 8; Indels
                                                                                                                            Query Match
Best Local Similarity 72.7%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 504 AA; 57711 MW; DFE306FD368EC59C CRC64;
                   InterPro; IPR000884; TSP1.
Pfam; PF00090; tSp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
SEQUENCE 388 AA; 39812 MW; CF493FD9C6CE6A62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical 57.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                          504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        search completed: February 11, 2003, 18:19:40
Job time : 26.5979 secs
                                                                                                                                                                                                                                                                                                                                                              PRT;
InterPro; IPR003067; Crcmsprzoite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 EAEXIXXXEEIVPNXVEQK 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity '
                                                                                                                                                                                                                                                   347 EEITPNDVEVK 357
                                                                                                                                                                                                                           11 EEIVPNXVEQK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                       Q8RWX2
                                                                                                                                                                                                                                                                                                                               RESULT 15
Q8RWX2
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| SIDS2/gcgdata/geneseq/geneseqp-emb1/Ak1991.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/Ak1992.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/Ak1992.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/Ak1994.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/Ak1995.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/Ak1995.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/Ak1996.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/Ak1999.DAT:*
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| SIDS2/gcgdata/geneseq/geneseqp-emb1/Ak2000.DAT:*
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| SIDS2/gcgdata/geneseq/geneseqp-emb1/Ak2001.DAT:*
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| SIDS2/gcgdata/geneseq/geneseqp-emb1/Ak2001.DAT:*
                                                                                                                                                                    February 11, 2003, 18:06:55; search time 36.3402 Seconds (without alignments) 91.669 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS2/gcgdata/geneseg/genesegp-embl/AA1990.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*/SIDS2/gcgdata/geneseq-geneseqp-emb1/AA1993.DAT:*/SIDS2/gcgdata/geneseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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12:
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                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                      Title:
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Anticariogenic pho	Casein phosphopepu	Sequence of casein	BOS Deta-casein A-	Metnyl or ecnyl es	BOVINE Deta casein	BOVINE Deca-casein	Phosphopeptide 2:	FIOSPIIOPEPLIAE **	Allereat rogente Piro
SUMMARIES		OI	AAR28425	AAR32927	AAR47814	AAW66600	AAR80281	AAR95609	AAB60348	AAP71321	AAR14448	AAR28427
		OB	13	14	15	19	16	17	22	ω	12	13
		Query Match Length DB ID	25	25	25	25	209	209	209	24	24	24
	æ	Query	96.2	96.2	96.2	96.2	96.2	96.2	96.2	91.4	91.4	91.4
		Score	101	101	101	101	101	101	101	96	96	96
		Result No.		10	, r	4	· LC	9	7	- σο	0	10

bhopping a sequence of the seq	pre-pro-VG1. Aeno Arabidopsis thalia Herbicidally activ Putative P. abyssi
24444 2444 24444 24444 24444 24444 24444 24444 24444 24444 24444 24444 2444 24	
991.4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	388.1
4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4444
11121111222222223333333333333333333333	14444 2444 5

ALIGNMENTS

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/note= "post-translationally phosphorylated serine"
                                                                                                                                                                                    --- "post-translationally phosphorylated serine"
                                                                                                                                            /note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                       ____nost-translationally phosphorylated serine"
                                                                                         Casein; metal ion; dietectic; purification; growth medium; dietary
                                                                                                                                                                                                                                                                                                                (UYME ) UNIV MELBOURNE. (VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                            Location/Qualifiers
              AAR28425 standard; peptide; 25 AA.
                                                                            Anticariogenic phosphopeptide.
                                                                                                                                                                                                                                                                         92WO-AU00175.
                                                                                                                                                                                                                                                                                               91AU-0005706.
                                                        19-MAR-1993 (first entry)
                                                                                                         supplement; fertiliser.
                                                                                                                                                                                                      Modified-site
                                                                                                                                          Modified-site
                                                                                                                                                              Modified-site
                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                19-APR-1991;
                                                                                                                                                                                                                                                                            16-APR-1992;
                                                                                                                                                                                                                                    WO9218526-A.
                                                                                                                                                                                                                                                      29-0CT-1992.
                                       AAR28425;
RESULT 1
AAR28425
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WPI; 1993-093685/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9400146-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JAN-1994,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reynolds EC;
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                  AAR47814;
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                  AAR47814
             δλ
                                                                                                                                                                                                                                                                        pp
                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                          The peptide may be prepd. by completely digesting casein in soln. with a proteolytic enzyme, adding mineral acid to the soln. to adding the 4 to 4 '', removing any precipitate, adding calcium schloride to cause aggregation of the peptides in soln. and separating the aggregated phosphopeptides. This method allows proof the phosphopeptide by industrial methods. The phosphopeptide has anticariogenic activity and may be used as a dietectic. The supplement or as a fertiliser. Supplement or as a fertiliser.
                                                                                                                                                                                                                                                                                                     Gaps
                                                   Selected phospho-peptide(s) prodn. having anticariogenic activities etc. - comprises digesting soluble monovalent cation salt of casein in soln., introducing di- or trivalent metal ion and filtering through filter having mol. wt. exclusion limit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Casein; phosphopeptide; dental calculus; salts; alkaline metal; alkaline earth metal; Zn/phosphopeptide complex; aggregate; anti-caries; anti-gingivitis.
                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                        Score 101; DB 13; Length 25;
Pred. No. 2.4e-10;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYME ) UNIV MELBOURNE.
(VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      AAR32927 standard; Protein; 25 AA.
                                                                                                                                                                                                                                                                                                               1 RELEEL,NVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                          Claim 11; Page 9; 18pp; English.
                                                                                                                                                                                                                                                                     96.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-0748344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92WO-AU00441
                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-1993 (first entry)
                                                                                                                                                                                                                                                                               Local Similarity 84.0 hes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Casein phosphopeptide #1.
                              WPI; 1992-382039/46.
                                                                                                                                                                                                                                                   25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
            Reynolds EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9303707-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reynolds EC;
                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                             AAR3292
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The sequences given in AAR32927-35 are casein phosphopeptides which can be used to inhibit dental calculus. These peptides are pref. in the form of salts selected from alkaline metal, alkaline earth metal salts such as Na, Ca, Zn, Cu, Al, K, Sr, Mg and Ni salts. These peptides peptides peptides have anti-calculus potential, and are anti-caries and anti-caries and anti-
                                                                                                                                                                                                                                                                                                         Gaps
Controlling dental calculus by treating teeth with oral compsns. which contains phospho-peptide(s) having 5-40 amino-acyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Casein phosphopeptide; dentinal hypersensitivity; therapy; tooth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ser(P) - post-translationally phosphorylated serine. A mixture of casein phosphopetides (CPP) and/or their salts may be used in a method for treating dentinal hypersensitivity. Pref. those CPPs contg. the sequence -Ser(P)-Ser(P)-Ser(P)- predominate. The CPPs can be extracted from a casein digest.
                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment of dentinal hypersensitivity - using casein, component of casein, phospho-protein or phospho-peptide or their salts
                                                                                                                                                                                                                                                            96.2%; Score 101; DB 14; Length 25;
84.0%; Pred. No. 2.4e-10;
Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Ser(P)
/note= "see also residues 17,18,19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of casein phosphopeptide (CPP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYME ) UNIV MELBOURNE.
(VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 11; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR47814 standard; peptide; 25 AA
                                                            Claim 3; Page 15; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93WO-AU00319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92AU-0003221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                       Best Local Similarity 84.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1994-025888/03.
                                                                                                                                                                                                                             25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
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25 AA;

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Gaps

; 0

4; Indels

Length 25;

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cats and dogs as well as zoo animals. The present sequence represents a phosphopeptide component of a specifically claimed complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "pepsin cleavage site in native protein and
in ethyl ester of beta-casein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "pepsin cleavage site in native protein and
in ethyl ester of beta-casein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "pepsin cleavage site in native protein and in ethyl ester of beta-casein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "pepsin cleavage site in native protein and in ethyl ester of beta-casein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "pepsin cleavage site in native protein and
in ethyl ester of beta-casein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "pepsin cleavage site in native protein and in methyl ester of beta-casein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "newly identified pepsin cleavage site in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "pepsin cleavage site in native protein"
126..127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "newly identified pepsin cleavage site in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "pepsin cleavage site in native protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "pepsin cleavage site in native protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "pepsin cleavage site in native protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "pepsin cleavage site in native protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ethanol, resulting in atypical pepsin
cleavage sites, in addition to the
naturally occurring (native) sites"
                                                                                                                                                                                                                                                                                                                                                          Bovine; beta-casein; ethyl esterification; pepsin hydrolysis; proteolysis; peptide ester; food; pharmaceutical; cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "55% esterified by methanol or by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                methyl ester of beta-casein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methyl ester of beta-casein
                                                                                                                                                                                                                                                                                                                                 Methyl or ethyl esterified bovine beta-casein Al.
                                                                             Score 101; DB 19;
pred. No. 2.4e-10;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                              AAR80281 standard; protein; 209 AA.
                                                                                                                                         1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                      1 RELEELNVPGEIVESLSSSEESITR 25
                                                                                   96.2%;
84.0%;
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                   Local Similarity 84.0° coservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                          25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cleavage-site
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                                                                                                                                                                                                                                                                                                              14-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus
                                                                                                                                                                                                                                                                                 AAR80281;
                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                        Query Match
                                                                                                                      Matches
                                                                                                                                                                                                                           RESULT 5
                                                                                                                                                                                                                                        AAR80281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FT
                                                                                                                                                                                                                                                                                   S S S S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a stable calcium phosphate complex including phosphopeptide stabilised amorphous calcium phosphate (ACP) or its christian phosphopeptide includes the amino acid sequence: derivative, where the phosphopeptide includes the amino acid sequence: Ser(P)-Ser(P)-Glu-Glu. The amorphous phases stabilised by the phosphopeptide for co-localisation of Ca, phosphopeptides are a delivery vehicle for co-localisation of Ca, and phosphate at the tooth surface in a slow-release amorphous form producing superior anticaries efficacy over prior art. The amorphous producing superior atticaries efficacy over prior art. The amorphous phosphopeptides are also useful as dietary phases stabilised by the phosphopeptides are also useful as dietary calcium cappelements to increase calcium deficiencies. They are particularly useful for treatment or prevention of dental caries, calcium cappelements of dental caries, calcium cappendicions are useful in humans and in veterinary medicine in the compositions are useful in humans and in veterinary medicine in the capp.
                                                                ö
                                                                                                                                                                                                                                                                                                                  casein; calcium phosphate complex; amorphous calcium phosphate; ACP; phosphopeptide; delivery vehicle; calcium fluoride; calcium deficiency; osteoporosis; osteomalacia; tooth; bone disease.
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stable calcium phosphate complex including phospho:peptide stabilised amorphous calcium phosphate - useful for treatment of dental caries, calcium malabsorption and bone diseases such as
                                                                     .
0
                                 Score 101; DB 15; Length 25;
pred. No. 2.4e-10;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                            Bos beta-casein X-4P (f1-25) phosphopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                        AAW66600 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 35; 43pp; English.
                                                                                                   1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                        /note= "Ser(P)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Ser(P)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Ser(P)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Ser(P)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteoporosis and osteomalacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-AU00160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97AU-0005662
                                            96.2%;
                                                                                                                                                                                                                                                                      (first entry)
                                                                          21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYME ) UNIV MELBOURNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-520803/44.
                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-1997;
                                                                                                                                                                                                                                                                        27-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                           AAW66600;
                                                 Query Match
                                                                               Matches
                                                                                                                                                                                     RESULT 4
                                                                                                                                                                                                 AAW66600
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/note= "pepsin cleavage site in native protein and in methyl and ethyl esters of beta-casein"
                                                                                                                                                                                                                 /note= "pepsin cleavage site in native protein and
in methyl and ethyl esters of beta-casein"
                                                                                                                                                                                                                                                          /note= "pepsin cleavage site in native protein and
in ethyl ester of beta-casein"
                                                                                                                                                                                                                                                                                                   /note= "pepsin cleavage site in native protein and
in methyl ester of beta-casein"
                                                                                                                                                                                                                                                                                                                                           /note= "pepsin cleavage site in native protein and in methyl and ethyl esters of beta-casein"
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "pepsin cleavage site in native protein and in methyl and ethyl esters of beta-casein"
                                                                                                                                                                                                                                                                                                                                                                                    /note= "pepsin cleavage site in native protein and
in ethyl ester of beta-casein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "pepsin cleavage site in native protein and in methyl and ethyl esters of beta-casein"
                                                                                                                           /note= "newly identified pepsin cleavage site in ethyl ester of beta-casein"
                                                                                                                                                                      /note= "newly identified pepsin cleavage site in ethyl ester of beta-casein"
                              "pepsin cleavage site in native protein"
                                                           /note= "pepsin cleavage site in native protein"
142..143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "newly identified pepsin cleavage site in methyl and ethyl esters of beta-casein"
/note= "pepsin cleavage site in native protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "newly identified pepsin cleavage site in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= A
/note= "tryptic peptide from native protein"
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/note= "tryptic peptide from native protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= D
/note= "tryptic peptide from native protein"
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/note= "tryptic peptide from native protein"
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/note= "tryptic peptide from native protein"
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/note= "tryptic peptide from native protein"
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/note= "tryptic peptide from native protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "note= "tryptic peptide from native protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methyl ester of beta-casein"
               127..128
                                            141..142
                                                                                                                                                                                                                                                                                                                                                                        190..191
                                                                                                                                                                                                                                                                                                                                                                                                                                                        192..193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207..208
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                                /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=
             Cleavage-site
                                         Cleavage-site
                                                                   Cleavage-site
                                                                                                             Cleavage-site
                                                                                                                                                       Cleavage-site
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                                                                                                                                                                                                                                          Cleavage-site
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The native form of bovine beta-casein Al contains various pepsin cleavage sites. Esterification of the protein with methanol or ethanol results in a form of beta-casein contg. additional, non-conventional pepsin cleavage sites (see Features Table). Esterified peptides and amino acids (and their mixtures) resulting from hydrolysis of an esterified protein (pref. beta-lactoglobulin or beta-casein) are claimed. The hydrolysis products are useful as ingredients, additives or active agents in foods, pharmaceuticals and cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   New esterified amino acids, peptide(s) and their mixts. - prepd. by esterification of protein then enzymatic hydrolysis, useful as ingredients and additives in foods, pharmaceuticals and cosmetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                             /label- L
/note= "tryptic peptide from native protein"
                                                                                /note= "tryptic peptide from native protein"
  /note= "tryptic peptide from native protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Milk; beta casein; diabetogenic; diabetes; cow; milk products;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.2%; Score 101; DB 16; Length 209;
84.0%; Pred. No. 3e-09;
tive 0; Mismatches 4; Indels
                                                                                                          /note= "phosphorylated"
                                                                                                                                       'note= "phosphorylated"
                                                                                                                                                                                                                     /note= "phosphorylated"
                                                                                                                                                                 /note= "phosphorylated"
                                                                                                                                                                                           /note= "phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Fig 7 and 18; 47pp; French.
                                                                                                                                                                                                                                                                                                                                                     (INRG ) INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR95609 standard; protein; 209 AA.
                                                                                                                                                                                                                                                                                                                                                                                Briand L, Chobert J, Haertle T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine beta casein Al variant.
                                                                                                                                                                                                                                                                                                                              93FR-0015764.
                                                                                                                                                                                                                                                                                                     94WO-FR01500
                                                                     /label= N
                 .202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            butter; cheese; cream.
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-240679/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 AA;
                                                                                           Modified-site
                                                                                                                     Modified-site
                                                                                                                                                 Modified-site
                                                                                                                                                                           Modified-site
                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                             WO9517518-A1
                                                                                                                                                                                                                                                                                                 20-DEC-1994;
                                                                                                                                                                                                                                                                                                                          23-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
                Peptide
                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR95609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              datches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
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The invention relates to a dietary supplement which, when consumed, cc is capable of reducing plasma levels of homocyst(e)ine (tHcy). tHcy is compared to reducing plasma levels of homocyst(e)ine (tHcy). tHcy is cc a major risk indicator of heart disease and vascular disease in general major risk indicator of heart disease and vascular disease in general cc factor for mortality in type II diabetic patients. Deficiencies in folic acid acid, pyridoxine and cobalamin lead to higher tHcy levels, and folic acid deficiency is known to be involved in vascular disease, as well as causing neural tube defects in early embryonic development. The causing neural tube defects in early embryonic development. The dietary supplement of the invention comprises milk or a milk product, dietary supplement of the invention comprises and milk product, cor their analogues. In addition, the beta-casein component of the milk is or their analogues. In addition, the beta-casein component of the milk is substantially the A2 variant. Beta-casein types A1 and B, consumption of substantially excluded from the supplement. The dietary supplement is useful for reducing the incidence of type I diabetes, are particularly excluded from the supplement. The dietary supplement is comparable and is also useful for reducing the incidence of type I and II.

C particularly cardiovascular disease and cerebrovascular disease, contable the additionally provides a sufficient daily dose of folic acid diabetes. It additionally provides a sufficient daily dose of folic acid contable improvements to a human population without the administration of medication. The present sequence represents bovine beta-casein type A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caries; gingivitis; periodontal disease; osteoporosis; osteomalacia.
                   prophylactic dietary supplement for reducing incidence of cardio, cerebro vascular diseases and diabetes in a population, contains milk or its products fortified with betaine, cobalamin, folic acid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.2%; Score 101; DB 22; Length 209; 84.0%; Pred. No. 3e-09; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP71321 standard; peptide; 24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87WO-AU00172
                                                                                                                Claim 9; Fig 3; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAY-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 21; Conserva
WPI; 2001-112363/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphopeptide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO8707616-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-DEC-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                      pyridoxine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP71321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine; beta-casein; type A2; milk; dairy product; dietary supplement; plasma homocysteine; homocystine; tHcy; folic acid; pyridoxine; betaine; cobalamin; vascular disease; diabetes; peripheral vascular disease; blood vessel wall degeneration; cardiovascular disease; cerebrovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                             Selecting non-diabetogenic milk and milk prods. - by testing milk or cows for the presence of non-diabetogenic variants of beta-casein
                                                                                                                                                                                                                                                                                                                                                                                                             A method for selecing milk for feeding to diabetes suscetible individuals comprises testing milk from identified cows for the presence of variants of beta casein and selecting those cows whose milk contains non-diabetogenic variants and milkking these cows separately. The milk and milk products obtained can reduce the risk of susceptible individuals contracting Type-1 diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.2%; Score 101; DB 17; Length 209; 84.0%; Pred. No. 3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                /label- Diabetogenic hexapeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NZMI-) NEW ZEALAND MILK INST LTD.
                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Figure 2; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB60348 standard; protein; 209 AA.
                                                                                                                                                                                                                   (NACH-) NAT CHILD HEALTH RES FOUND. (NZDA-) NEW ZEALAND DAIRY BOARD.
                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RELEELNVPGEIVESLSSSEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-1999; 99NZ-0336505.
18-APR-2000; 2000NZ-0504057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-2000; 2000WO-NZ00116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovine beta-casein type A2.
                                                                                                                                                          95WO-NZ00114.
                                                                                                                                                                                        94NZ-0264862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elliott RB, Laugesen BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 84.03
Matches 21; Conservative
                                                                                                                                                                                                                                                                         Elliott RB, Hill JP;
                                                                                                                                                                                                                                                                                                           WPI; 1996-251885/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200100047-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-APR-2001
                                                                                                                                                           03-NOV-1995;
                                                                                                                                                                                          04-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
                                                                                         WO9614577-A1
                                                                                                                           17-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB60348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
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Gaps

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Novel phosphopeptides - useful for treating dental diseases, rarefying diseases or diseases relating to malabsorption of minerals
                                                                                              This is an example of a highly generic formula for a phosphopeptide of length 5-13 amino acids. The peptides can be made synthetically (e.g. chemical synthesis or genetic engineering) or they can be extracted from cereals, nuts or vegetables or by fractionating a compositions comprising the peptide may take the form of foodstuff topical application to teeth or gingival tissue. The peptides impulmentable application to teeth or gingival tissue. The peptides significantly increase absorption of calcium, phosphate and iron in the gut. See AAR14447-R14451.
                                                                          Claim 1; Column 11; 8pp; English.
                                                                                                                                                                                                                                                                                              2 ELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                          Conservative
                   WPI; 1991-316875/43.
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9218526-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reynolds EC;
                                                                                                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                  AAR28427;
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                  ;
0
                                                                                                                            New phosphopeptides contg. defined aminoa cid sequence - useful in treatment of dental, rarefying bone diseases and disease relating to malabsorption of minerals.
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         caries; gingivitis; periodontal disease; osteoporosis; osteomalacia;
                                                                                                                                                                                              The phosphopeptide is used in compsns. at a conc. of 0.01-5 wt%.
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                         Score 96; DB 8; Length 24;
Pred. No. 1.6e-09;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphopeptide #2 for increasing mineral absorption.
                                  (VICT-) VICTORIA DAIRY INDUSTRY AUTHORITY. (UYME-) UNIVERSITY OF MELBOURNE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "phosphoserine (Pse)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               AAR14448 standard; Protein; 24 AA.
                                                                                                                                                                                                                                                                                                  2 ELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                       Claim 5; Page 17; 22pp; English.
                                                                                                                                                                                                                                                                                                                (VICT-) VICTORIAN DAIRY INDUSTRY
               86AU-0006385.
                                                                                                                                                                                                                                                          91.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Pse"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Pse"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Pse"
                                                                                                                                                                                                          See also AAP71320-P71324.
                                                                                                                                                                                                                                                                                                                                                                                                                           10-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90US-0563798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90US-0563798.
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYME-) UNIV OF MELBOURNE,
                                                                                                    WPI; 1987-362707/51.
                                                         (REYN/) EC REYNOLDS
                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                  24 AA;
             12-JUN-1986;
                                                                                 Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                                                                                                                                                                                                             20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      AAR14448;
                                                                                                                                                                                                                                                                            Matches
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Gaps

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Length 24;

91.4%; Score 96; DB 12; Length 24 83.3%; Pred. No. 1.6e.09; tive 0; Mismatches 4; Indels

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/note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                 /note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                     _note= "post-translationally phosphorylated serine"
                                                                                                                                                 Casein; metal ion; dietectic; purification; growth medium; dietary supplement; fertiliser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Selected phospho-peptide(s) prodn. having anticariogenic activities etc. - comprises digesting soluble monovalent cation salt of casein in soln., introducing di- or trivalent metal ion and filtering through filter having mol. wt. exclusion limit
                                                                                                                                                                                                                                                                                                                                                                                            (VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                    Location/Qualifiers
                                                          AAR28427 standard; peptide; 24 AA.
1 ELEELNVPGEIVESLSSSEESITR 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 11; 18pp; English.
                                                                                                                          Anticariogenic phosphopeptide.
                                                                                                                                                                                                                                                                                                                                       92WO-AU00175.
                                                                                                                                                                                                                                                                                                                                                            91AU-0005706.
                                                                                                     19-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                (UYME ) UNIV MELBOURNE.
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAR32927-35 are casein phosphopeptides which can be used to inhibit dental calculus. These peptides are pref. in the form of salts selected from alkaline metal, alkaline earth metal salts
                                                                                                                                                                   .;
0
       The peptide may be prepd. by completely digesting casein in soln.

with a proteolytic enzyme, adding mineral acid to the soln. to
adjust the pH to 4.7, removing any precipitate, adding calcium
adjust the pH to 4.7, removing any precipitate, adding calcium
chloride to cause aggregation of the peptides in soln. and
separating the aggregated phosphopeptides. This method allows prodn.
of the phosphopeptide by industrial methods. The phosphopeptide
has anticariogenic activity and may be used as a dietectic. The
peptide may be used in a microbiological growth medium, as a dietary
supplement or as a fertiliser.
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Controlling dental calculus by treating teeth with oral compsns. - which contains phospho-peptide(s) having 5-40 amino-acyl
                                                                                                                                                                                                                                                                                                                                           Casein; phosphopeptide; dental calculus; salts; alkaline metal; alkaline earth metal; Zn/phosphopeptide complex; aggregate; anti-caries; anti-qingivitis.
                                                                                                                                                                     ;
0
                                                                                                                                               91.4%; Score 96; DB 13; Length 24; 83.3%; Pred. No. 1.6e-09; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 16; 23pp; English.
                                                                                                                                                                                                                                                                   AAR32929 standard; Protein; 24 AA.
                                                                                                                                                                                             2 ELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                         92WO-AU00441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91US-0748344.
                                                                                                                                                                                                                                                                                                              02-JUL-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                   Casein phosphopeptide #3.
                                                                                                                                                             Query Match
Best Local Similarity 83.3°
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYME ) UNIV MELBOURNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-093685/11.
                                                                                                                 See also AAR28425-33.
                                                                                                                                       24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9303707-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residues
                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                               AAR32929;
                                                                                                                                       Sequence
                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                AAR32929
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The sequences given in AAR31237-42 represent phosphopeptides which were used as the active agents in an oral composition. These peptides were stabilised by an anionic polymeric stabiliser. The anionic polymers were chosen from a group consisting of carboxylate polymers, sulfonate polymers, polymers having both a carboxylate and polymers, sulfonate moiety, and other such mixtures. The anionic polymeric a stabiliser inhibits destabilisation of the phosphopeptide in the oral stabiliser inhibits destabilisations, pref. containing a fluoride source may be used for inhibiting caries and gingivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphopeptide; active agent; oral; composition; anionic; polymeric; stabiliser; carboxylate; polymer; sulfonate; destabilisation; fluoride; caries; gingivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oral compsns. contg. a phospho:peptide - with addn. of an anionic polymeric stabiliser to inhibit destabilisation in the oral
such as Na, Ca, Zn, Cu, Al, K, Sr, Mg and Ni salts. These peptides are pref. present as a Zn/phosphopeptide complex or aggregate. these peptides have anti-calculus potential, and are anti-caries and anti-
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                 ;
0
                                                                                                                                                                91.4%; Score 96; DB 14; Length 24; 83.3%; Pred. No. 1.6e-09;
                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label= Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burger AR, Elliott DL, Schick LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 14; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               AAR31238 standard; peptide; 24 AA.
                                                                                                                                                                                                                                                                      2 ELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                 92EP-0202023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-0731592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAY-1993 (first entry)
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-019802/03
                                                                                                                                                                                                            Local Similarity
                                                                                                 gingivitis agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphopeptide 2.
                                                                                                                                               24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      environment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP523776-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic.
                                                                                                                                                                                                                                           50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR31238;
                                                                                                                                                    Sequence
                                                                                                                                                                                           Query Match
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24 AA;

Sequence

g

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Phosphopeptide; tryptic digestion; sodium caseinate; alpha(s1)-caseinate; phosphoserine; phosphothreonine; phosphotyrosine; phosphohistidine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                         Casein phosphopeptide; dentinal hypersensitivity; therapy; tooth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ser(P) = post-translationally phosphorylated serine. A mixture of casein phosphopeptides (CPP) and/or their salts may be used in a method for treating dentinal hypersensitivity. Pref. those CPPs contg. the sequence -Ser(P)-Ser(P)-Ser(P)- predominate. The CPPs can be extracted from a casein digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Treatment of dentinal hypersensitivity – using casein, component of casein, phospho-protein or phospho-peptide or their salts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                               /label= Ser(P)
/note= "see also residues 16,17,18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.4%; Score 96; DB 15;
83.3%; Pred. No. 1.6e-09;
ilve 0; Mismatches 4;
                                                                                                                                                      Sequence of casein phosphopeptide (CPP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sodium caseinate tryptic phosphopeptide T2.
                                                                                                                                                                                                                                                                                                                                                                                (VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                   AAR47816 standard; peptide; 24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 13; 23pp; English.
         2 ELEELNVPGEIVEXLXXXEESITR 25
                       AAR68937 standard; Peptide; 24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93WO-AU00319.
                                                                                                                                                                                                                                                                                                                                                 92AU-0003221.
                                                                                                                               21-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                    (UYME ) UNIV MELBOURNE.
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-025888/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 AA;
                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                        29-JUN-1993;
                                                                                                                                                                                                                                                                           WO9400146-A.
                                                                                                                                                                                                                                                                                                                                              29-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                     Reynolds EC;
                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR68937;
                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                             Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The peptide sequence is that of a phosphopeptide prepd. from a tryptic digest of casein. The peptide may be used with an anticaludus agent, e.g. alkali metal pyrophosphate, in a compsn. for brushite and amorphous calcium phoshphate into the more stable hydroxyapatite on the teeth. The compsn. is used in the form of amouthwash. toothpaste, gel, lozenge or chewing gum, for care of the See also AAR32308-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phospho-peptide(s) for dental tartar control - are included in compsns. with pyrophosphate(s) or zinc salts to provide good
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
          91.4%; Score 96; DB 14; Length 24;
83.3%; Pred. No. 1.6e-09;
tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                   /note= "post-translationally phosphorylated"
                                                                                                                                                                                                                                                                                                                         /hote= "post-translationally phosphorylated"
                                                                                                                                                                                                                                                                                                                                               'note= "post-translationally phosphorylated"
                                                                                                                                                                                                                     Dental, teeth; tartar control; brushite; calcium phosphate; hydroxyapatite; mouthwash; toothpaste.
                                                                                                                                                                                                                                                                                                                                                                     /note= "post-translationally phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.4%; Score 96; DB 14; Length 24;
83.3%; Pred. No. 1.6e-09;
tive 0; Mismatches 4; Indels
                                                                                                                                                                                                Phosphopeptide derived from casein.
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                            AAR32309 standard; peptide; 24 AA.
                                                  2 ELEELNVPGEIVEXLXXXEESITR 25
                                                                Claim 3; Page 12; 17pp; English.
Query Match
Best Local Similarity 83.3%
Watches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      92EP-0202024.
                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           91GB-0017315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 83.3
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burger AR, Schick LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNIL ) UNILEVER PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNIL ) UNILEVER NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-060322/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 AA;
                                                                                                                                                                                                                                                                                      Modified-site
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                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                           10-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-1993.
                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                       EP528458-A.
                                                                                                                                                    AAR32309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                        RESULT 13
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peptides (AAR68936-40) are phosphopeptides resulting from the tryptic digestion of sodium caseinate. The peptide shown here is derived from the TCPK-tryptic digest of beta-caseinate. The peptides contain the amino acids phosphoserine, phosphothreonine, phosphotyrosine or phosphopeptides, and include in their sequence aspartate and glutamate. The phosphopeptides form part of a novel composition containing the peptide dispersed uniformly in a crystal mix of sugars chosen from peptide dispersed uniformly in a crystal mix of sugars chosen from sorbitol, mannitol, xylitol, lacticol, cellobiitol or mixtures of sorbitol, mannitol or sorbitol/xylitol. The compositions can be used sorbitol/mannitol sugars to manufacture confectionary products. Instead of conventional sugars to manufacture confectionary products. The phosphopeptides are known to inhibit caries and gingivitis and can act as a source of calcium ions to promote/enhance remineralisation.
sugar; sorbitol; mannitol; xylitol; lactitol; cellobiitol; confectionary;
caries; gingivitis; calcium; remineralisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          crystalline poly:ol compositions for use in confectionery and pharmaceuticals - contain a phospho:peptide uniformly distributed within the crystal matrix and can improve oral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 1 Similarity 83.3%; pred. No. 1.6e-09; 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                           note= "Phosphoserine"
                                                                                                                                                                                                                                                                         /note= "Phosphoserine"
                                                                                                                                                                                  'note= "Phosphoserine"
                                                                                                                                      'note= "Phosphoserine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; column 4; 8pp; English.
                                                                           Location/Qualifiers
14
                                                                                                                                                                                                                                                           /label= OTHER
                                                                                                                                                                                                                 /label- OTHER
                                                                                                                                                                     /label= OTHER
                                                                                                                           /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                               93US-0078706.
                                                                                                                                                                                                                                                                                                                                                                    94EP-0304083.
                                                                                                                                                                                                                                                                                                                                                                                                                               (ICIL ) ICI AMERICAS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-044845/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 AA;
                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                          Modified-site
                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                    16-JUN-1993;
                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                           21-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                               EP629393-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duross JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                    Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hygiene
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Gaps 0

Search completed: February 11, 2003, 18:16:54 Job time : 37.3402 secs

2 ELEELNVPGEIVEXLXXXEESITR 25

Local Similarity

Matches

δλ

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February 11, 2003, 18:14:31 ; Search time 12.3711 Seconds (without alignments) 59.459 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                    105
1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                     262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                        US-09-380-738A-2
                                                                                                                                                                                                                                                                                              Scoring table: BLOSUM62
                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                      Run on:
                                                                                                                                                                                                                     Title:
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Issued_Patents_AA:*

Database :

SUMMARIES

Appli , Appl Appli Appl Appl Appli Appli Appli Sequence 6, Appli Sequence 4794, Ap Appl Appli Sequence 265, App Sequence 3, Appli Appli Appli Appli Appli Appli Appli Appli Appl Sequence 1, Appli Sequence 1, Appli , Appli Sequence 3, 1 Sequence 18, Sequence 13, Sequence 13, Sequence 13, Sequence 2, Sequence 13 Sequence 2, Sequence 4 Sequence 3 Sequence 3 Sequence 1 Sequence 2 Sequence 3 Description Sequence 2 Sequence Sequence Sequence Sequence Sequence Sequence US-08-078-090-2 US-09-453-702B-265 US-08-537-210A-3 US-09-113-825-3 US-08-185-432-18 US-09-134-001C-4794 US-08-391-743A-2 US-09-143-155-2 US-09-131-028A-2 US-09-131-028A-12 US-09-131-028A-12 US-08-868-786-6 US-08-889-419-13 US-08-402-542-13 PCT-US93-07189-13 US-08-954-985A-3 US-08-137-086-3 US-08-621-564B-1 US-09-269-220-1 US-08-137-086-1 US-09-269-220-2 US-08-836-778-2 US-07-748-344B-3 US-08-459-346-13 US-08-411-607A-4 US-08-954-985A-1 Query Match Length DB 441 440 440 330 330 330 Score Š. Result

NAME/KEY: Phosphoserine

Sequence 3, Appli Sequence 10. Appli Sequence 1, Appli Sequence 2, Appli Sequence 22, Appli Sequence 21, Appli Sequence 21, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 6, Appli
US-08-899-232-3 US-08-134-001C-5016 US-09-414-436-1 US-08-341-555-3 US-08-341-555-22 US-08-341-555-22 US-08-341-555-21 US-08-341-555-21 US-08-341-555-21 US-08-341-555-21 US-08-341-555-21 US-08-341-555-21 US-08-341-555-21 US-08-341-555-21 US-08-999-811-5 US-08-999-811-5 US-08-999-811-5 US-08-999-811-5 US-08-998-811-5 US-08-998-811-5 US-08-998-811-5 US-08-998-811-5 US-08-998-811-5 US-09-998-811-5 US-09-998-81-10-5 US-09-998-81-10-5 US-09-998-81-10-5 US-09-998-81-10-5 US-09-998-81-10-5 US-09-998-81-10-5 US-09-998-81-10-5 US-08-998-81-10-5 US-08-988-81-10-5 US-08-988-81-10-5 US-08-988-81-10-5 US-08-988-81-10-5 US-08-988-81-10-5 US-08-988-81-10-5 US-08-988-81-10-5 US-08-988-
444404441000004400
2523 270 271 271 271 21 51 54 196 196 196 196 196 196
339 337 337 337 337 337 337 337 337 347
80001000000000000000000000000000000000

ALIGNMENTS

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OTHER INFORMATION: Post-translationally phosphorylated serine OTHER INFORMATION:
                                                                                               TITLE OF INVENTION: PHOSPHOPEPTIDES FOR THE TITLE OF INVENTION: TREATMENT OF DENTAL CALCULUS
                                                                                                                                                                  ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL STREET: 100 EAST WISCONSIN AVE., SUITE 1100 CITY: MILWAUKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.8493-87
                                                                                                                                                                                                                                                                                                                                                                                         US/07/748,344B
                                                                                                                                                                                                                                                                                                                      IBM PC COMPATIBLE SYSTEM: PC-DOS/MS-DOS
                                                                                APPLICANT: REYNOLDS, ERIC CHARLES
RESULT 1
US-07-748-344B-1
Sequence 1, Application US/07748344B
Patent No. 5227154
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: C 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-2022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (608) 255-2022
TELEFAX: (608) 255-2182
TELEKX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30,4
                                                                                                                                                                                                                                                                                                     FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Phosphoserine
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
                                                                                                                                                                                                                                                                                                                                                                                                            19910822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
                                                                                                                                        NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                  WISCONSIN: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                    53202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                    STATE:
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0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Han, Sang Kee
APPLICANT: Han, Son Cheol
TITLE OF INVENTION: CASEIN PHOSPHOPEPTIDE, CASEIN CONTAINING
TITLE OF INVENTION: SAME, AND PROCESS FOR THE PREPARATION THEREOF
CORRESPONDENCE ADDRESS:
             OTHER INFORMATION: POSt-translationally phosphorylated serine
                                                                                     LOCATION: 18 OTHER INFORMATION: POSt-translationally phosphorylated serine
                                                                                                                                                                                               ) OTHER INFORMATION:

OTHER INFORMATION: Post-translationally phosphorylated serine

US-07-748-344B-1
                                                                                                                                                                                                                                                                         96.2%; Score 101; DB 1; Length 25; 84.0%; Pred. No. 2.7e-10; tive 0; Mismatches 4; Indels
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84.0%; Pred. No. 2.7e-10;
tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: Lowe, Price, LeBlanc & Becker
: 99 Canal Center Plaza, Suite 300
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/621,564B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 2438-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 684-1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08621564B Patent No. 5834427 GENERAL INFORMATION:
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                                                                                                                                                              NAME/KEY: Phosphoserine
                                                                                                                                                                                                                                                                                                          21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 684-1124
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                         Local Similarity
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Best Local Similarity
LOCATION: 17
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                                                                                                                                                                                  LOCATION:
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                                                                                                                                                                                                                                                                       Query Match
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OTHER INFORMATION: Post-translationally phosphorylated serine
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OTHER INFORMATION: Post-translationally phosphorylated serine
                                                                                                                                                                     ADDRESSEE: Dental School, The University of Melbourne STREET: 711 Elizabeth Street CITY: Melbourne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.2%; Score 101; DB 2; Length 25; 84.0%; Pred. No. 2.7e-10; tive 0; Mismatches 4; Indels
                                                                                            APPLICANT: REYNOLDS, Eric Charles
TITLE OF INVENTION: A Treatment for Sensitive Teeth
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/954,985A
FILLING DATE: 21-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21-OCT-1997
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,479
FILING DATE: 22-FEB-1995
ATOWNEY/AGENT INFORMATION:
NAME: WOZNY, THOMAS M
REGISTRATION NUMBER: 28,922
                                      ; Sequence 1, Application US/08954985A ; Patent No. 5981475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RELEBLINVPGEIVEXLXXXEESITR 25
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MEDIUM TYPE: Diskette
COMPUTER: IBM
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION: (414) 271-7590: TELEFAX: (414) 271-7590: INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/08137086
; Patent No. 6448374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 271-7590
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                     Australia
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TOPOLOGY: Linear
                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                     Victoria
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RESULT 3
US-08-954-985A-1
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Matches
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OTHER INFORMATION: Post-translationally phosphorylated serine
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REYNOLDS, ERIC CHARLES FROM CASEIN VENTION: PRODUCTION OF PHOSPHOPEPTIDES FROM CASEIN
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                                                             CORRESPONDENCE ADDRESS:
CORRESPONDENCE ANDRESS:
ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL
STREET: 100 EAST WISCONSIN AVE., SUITE 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPRENCE/DOCKET NUMBER: C.8493-87
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-2022
TELERX: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,086
FILING DATE: 04-MAR-1994
FILING DATE: 0530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RELEELNVPGEIVEXLXXXEESITR 25
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; Sequence 2, Application US/09269220
; Patent No. 6180761
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30,492
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84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                          FILING DATE: 04-MAR-1 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
                                                                                             STREET: 100 E.C. CITY: MILWAUKEE
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                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid
           APPLICANT: REYNOLDS TITLE OF INVENTION:
                                                                                                                                                             USA
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                                                                                                                                                         COUNTRY:
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Sequence 2, Application US/08836778
Sequence 2, Application US/08836778
GENERAL INFORMATION:
APPLICANT: ELLIOTT, ROBERT BARTLETT
APPLICANT: HILL, JEREMY PAUL
TITLE OF INVENTION: METHOD OF SELECTING NON-DIABETOGENIC MILK OR MILK
TITLE OF INVENTION: METHOD OF SELECTING NON-DIABETOGENIC MILK OR MILK
TITLE OF INVENTION: PAPOLOTYS AND MILK OR MILK PRODUCTS SO SELECTED
TITLE OF INVENTION: PAPEL 1995-11-03
CURRENT APPLICATION NUMBER: US_264862
PRIOR FILING DATE: 1994-11-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 2
LENTH: 209
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GENERAL INFORMATION:
APPLICANT: HAN, Sang K
APPLICANT: SHIN, YOO C
TITLE OF INVENTION: CASEIN AND PROCESS FOR THE PREPARATION THEREOF
FILLE REPERENCE: 1423.1001/MJH
CURRENT APPLICATION NUMBER: US$/09/269,220
CURRENT APPLICATION NUMBER: 1999-03-23
PRIOR PILING DATE: 1996-03-23
PRIOR FILING DATE: 1996-03-23
PRIOR FILING DATE: 1997-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence:BOVINE MILK COTHER INFORMATION: PROTEIN US-08-836-778-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 15.2%; Score 101; DB 4; Length 209; Il Similarity 84.0%; Pred. No. 3.1e-09; Some 21; Conservative 0; Mismatches 4; Indels
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APPLICATE: RENOLDS, ERIC CHARLES
TITLE OF INVENTION: PHOSPHOPEPTIDES FOR THE
TITLE OF INVENTION: TREATMENT OF DENTAL CALCULUS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/07748344B Patent No. 5227154
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Bos taurus
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                                                                                                                                                                                                                                                                                                                              SOFTWARE: Pat. SEQ ID NO 2 LENGTH: 209
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US-08-836-778-2
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STREET:
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OTHER INFORMATION: Post-translationally phosphorylated serine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.4%; Score 96; DB 1; Length 24; 83.3%; Pred. No. 1.7e-09; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATURE TRYOUDS, Eric Charles
TITLE OF INVERTION: A Treatment for Sensitive Teeth
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dental School, The University of Melbourne
: 100 EAST WISCONSIN AVE., SUITE 1100 MILWAUKEE
                                                                                                                                                                                   APPLICATION NUMBER: US/07/748,344B
FILING DATE: 19910822
                                                                                                                                                                                                                                                                                                                                                 C.8493-87
                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08954985A Patent No. 5981475
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30,492
REBRENCE/DOCKET NUMBER: C.8
TELECOMMUNICATION
TELEPHONE: (608) 255-2022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (608) 255-2022
TELERAX: (608) 255-2182
TELES: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO. 3:
SEQUENCE CHARACTERISTICS:
                                                                                                         FLOPPY DISK
                                                                                                                                               SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Phosphoserine LOCATION: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Phosphoserine
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                                                                                                                                                                                                FILING DATE: 19910822
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: Protein
                                  WISCONSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                         FILING DATE:
                                                                   53202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-748-344B-3
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                                  STATE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: Phosphoserine
; LOCATION: 18
; OTHER INFORMATION: Post-translationally phosphorylated serine
US-08-954-985A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Post-translationally phosphorylated serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: REYNOLDS, ERIC CHARLES
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
9
CORRESPONDENCE ADDRESS:
ADDRESSE: ANDRUS, SCEALES, STARKE & SAWALL
STREET 100 BAST WISCONSIN AVE., SUITE 1100
STATE: WISCONSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.4%; Score 96; DB 2; Length 24; 83.3%; Pred. No. 1.7e-09; tive 0; Mismatches 4; Indels
                                                                                                                                             OPERATING CASTI SOFTH ASCII CURRANE: ASCII CURRAN APPLICATION DATA: APPLICATION NUMBER: US/08/954,985A
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,479
FILING DATE: 22-FEB-1995
ATTORNEY AGENT INFORMATION:
711 Elizabeth Street
                                                                                                                             COMPUTER: IBM
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                        INFORMATIONE: (414) 271-7590: TELEFAX: (414) 271-7590: SEQUENCE CHARACTERISTICS: LENGTH: 24
TYPE: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ELEELNVPGEIVEXLXXXEESITR 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08137086 Patent No. 6448374 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  NAME: WOZDY, Thomas M
REGISTRATION NUMBER: 28,922
REFERENCE/DOCKET NUMBER: 32;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Phosphoserine
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                                                                                                                 Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                 Victoria
: Australia
                 Melbourne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                     COUNTRY: ZIP: 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53202
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linear
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                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-621-564B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Sequence 1, Application US/08621564B
Patent No. 5834427
GENERAL INFORMATION:
APPLICANT: Han, Sang Kee
APPLICANT: Shin, Yoo Cheol
TITLE OF INVENTION: CASEIN PHOSPHOPEPTIDE, CASEIN CONTAINING
TITLE OF INVENTION: SAME, AND PROCESS FOR THE PREPARATION THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-translationally phosphorylated serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Post-translationally phosphorylated serine OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-translationally phosphorylated serine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 91.4%; Score 96; DB 4; Length 24; Local Similarity 83.3%; Pred. No. 1.7e-09; es 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Lowe, Price, LeBlanc & Becker STREET: 99 Canal Center Plaza, Suite 300 CITY: Alexandria
                                                                                                                                                             APPLICALLO.

FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: C.8493-87
TELEPHONE: (608) 255-2022
TELEPHONE: (608) 255-2182
TELERAX: 26832 ANDSTRAK
; INFORMATION FOR SEC ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
Amino acid
                                                                   APPLICATION NUMBER: US/08/137,086
FILING DATE: 04-MAR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ELEELNVPGEIVESLSSSEESITR 24
IBM PC COMPATIBLE SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Phosphoserine
                                   SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: Amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 16
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
    COMPUTER: IBM PC (OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
HS-08-621-564B-1
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APPLICANT: HAN, Sang K
APPLICANT: HAN, YOOG
INTERORY INVENTION: CASEIN AND PROCESS FOR THE PREPARATION THEREOF
FILE OF INVENTION: CASEIN AND PROCESS FOR THE PREPARATION THEREOF
FILE PERENEWE: 1423.1001/MJH
CURRENT FILING DATE: 1999-03-23
CURRENT APPLICATION NUMBER: US/09/269,220
CURRENT APPLICATION NUMBER: PCT/KR97/00182
PRIOR FILING DATE: 1996-03-23
PRIOR FILING DATE: 1997-09-23
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.4%; Score 96; DB 4; Length 209; 83.3%; Pred. No. 2.1e-08; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
COMPUTER REDABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,564B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 91.4%; Score 96; DB 2; I
Best Local Similarity 83.3%; Pred. No. 2.1e-09;
Matches 20; Conservative 0; Mismatches 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: phospholyated serine NAME/KEY: ACT_SITE LOCATION: (17)..(19)
                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFENCE/DOCKET NUMBER: 2438-022
TELEPHONE: (703) 684-1111
TELEPHONE: (703) 684-1114
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RELEELNVPGEIVEXLXXXEESIT 24
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US-09-269-220-1
Sequence 1, Application US/09269220
; Patent No. 6180761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                  CLASSIFICATION: 514
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Best Local Similarity
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                                                                                                APPLICANT: Difullio, Paul A.; Meade, Harry; Cole, Edward S.
TITLE OF INVENTION: TRANSGENETICALLY PRODUCED ANTITHROMBIN III
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/143,155
                                                                                                                                                                                                                                                                                       COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/391,743A FILING DATE: 21-FEB-1995
                                     ; Sequence 2, Application US/08391743A
; Patent No. 5843705
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RELEELNVPGEIVEXLXXXEESIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09143155
Patent No. 6441145
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TC.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Myers, Paul Louis
REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 222 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 72.4%
Best Local Similarity 70.8%
Matches 17; Conservative
                                                                                                                                                                                                                                         Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-391-743A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                  Boston
                                                                                                                                                                                                                                                                             02109
              US-08-391-743A-2
                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                     STATE:
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 72.4%; Score 76; DB 4; Length 222 Best Local Similarity 70.8%; Pred. No. 4.3e-05; Matches 17; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Lemmel, Steven A.
APPLICANT: Lemmel, Steven A.
APPLICANT: Lemmel, Steven A.
APPLICANT: Chaudhary, Sunita
TILE OF INVENTION: BETA-CASEIN EXPRESSING CONSTRUCTS
FILE REFERENCE: 6004.0S.Pl
CURRENY APPLICATION NUMBER: US/09/131,028A
CURRENY FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: US 08/064,440
                                                                                                                                                       REFERENCE DOCKET NUMBER: TCI-045
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/391,743
                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                     NAME: Myers, Paul Louis
REGISTRATION NUMBER: 35,965
                     CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Lemmel, Steven A.
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Chaudhary, Sunita
FILING DATE: 28-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/09131028A ; Patent No. 6287866
                                                                                                                                                                                                                                                                               LENGTH: 222 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 12, Application US/09131028A ; Patent No. 6287866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RELEELNVPGEIVEXLXXXEESIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 REQEELNVVGETVESLSSSEESIT 39
                                                                                   FILING DATE: <Unknown>
                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 VPGEIVEXLXXXEESIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-131-028A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-131-028A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-131-028A-12
                                                                                                                                                                                                                                                                                                                                                                                US-09-143-155-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: February 11, 2003, 18:19:51; Search time 12.1134 Seconds (without alignments)
52.729 Million cell updates/sec

Title: US-09-380-738A-2
Ferfect score: 105
Sequence: 1 RELEELNYPGEIVEXLXXXEESITR 25
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 140259 seqs, 25548876 residues
```

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 se : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_WEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/PCT_WEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 38, Appl	Sequence 8, Appli	Sequence 3, Appli	Sequence 14025, A	Sequence 5720, Ap	Sequence 4, Appli	Seguence 265, App	Sequence 4814, Ap	Sequence 4, Appli	Segmence 28. Appl	Tale (or concerned	Sednence 40, Whit	Seguence 50, Appl	Sequence 7, Appli	Secmence 5, Appli		٠,	Sequence 3, Appl1	Segmence 125, App	,	Sequence 3, Appli	Sequence 14, Appl	•
	ΩI	US-09-110-716-38	US-09-934-054-8	US-09-991-258-3	US-09-815-242-14025	US-09-738-626-5720	US-09-361-741-4	ris-10-114-170-265	115-09-738-626-4814	10-00-767-70A-4	107 CO CO CO	US-09-893-519A-20	US-09-853-450-40	rrs-09-853-450-50	ns-10-060-523-7	H-3CE-3CO OF CO	05-03-256-50	US-10-084-488-5	TIC-00-749-728B-3	10 10 10 10 10 10 10 10 10 10 10 10 10 1	US-08-785-006A-175	US-10-127-551-3	TTG-00-850-000A-14	03 03 032 202 20
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dР	Query Match 1	41.0	41.0	77.0		0.0	0.00		57.T	1.70	36.2	36.2	35.2	25.0	9 0	30.6	35.2	35.2		30.7	35.2	35 2		35.2
	Score	43	7 *	7 7	, <u>,</u>	7 -	+ C	2 0	א ני	n (38	38	37		o t	3/	37	3.7	2 0	3/	37	37		37
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-	Sequence 4, Appli	Sequence 133137 ::	Sequence 133. App	Seguence 2. Appli	Segmence 28, Appl	Segmence 4. Appli	Sequence 1540. Ap	Sequence 3644 An	Sequence 30447	Seducinice 13400	Sednence 3935, Ap	◂	Sequence 4, Appli	Sequence 4, Appli	Segmence 2. Appli	Sequence 2. Appli	i lade c economic	seducino via appre		Sequence 12668, A	Sequence 266, App	Segmence 13646, A		1 7 7	sednence 13, Appr
US-09-712-363-196 US-10-045-792-11 US-10-045-792-10	US-09-272-809-4	US-09-864-761-43315	US-09-904-568-2	US-10-114-893-133	US-U9-884-366-2	US-10-042-41/-20	US-09-918-951-4	US-09-86/-550-T340	US-09-738-626-3644	US-09-815-242-13405	US-09-738-626-3935	118-09-866-582-42	TC-10-217-357-4	115 OF 117 OF 110 OF 11	US-03-3/3 320 *	US-09-934-406-2	US-10-21/-35/-2			ris-09-815-242-12668		20 00 01E-040-13646	US-U9-813-242-13040	US-08-828-811	US-09-924-154-13
თთσ	10	10	10	σ,	5	17	10	10	σ	10	6	, (4 0	ν .	7	σ	6	10	10		1 -	9 6	10	10	10
389 786 793	1371	84	224	387	521	621	640	642	647	750	755	760	207	00/	(0/	166	992	992	794		200	1014	1226	1242	1421
35.2	35.2	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	2 7 6		0.40	34.3		34.3	34.3	34.3	2 / 3			34.3	34.3	34.3	34.3
37	37	36	36	36	36	36	36	36	36	. ~	9 6	000	200	36	36	36	36	7	9 0	0 (0 1	36	36	36	36
20 21	222	24	25	26	27	28	58	30	3.	3.2	7 (55	34	32	36	37	88	0 0	1 5	0 1	41	42	43	44	45

ALIGNMENTS

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0; Gaps
Sequence 38 Application US/09110716A
| Sequence 38 Application US/09110716A
| Patent No. US20020034739A1
| GENERAL INFORMATION:
| APPLICANT: Lefter. Robert I. APPLICANT: Zhao, Chengquan APPLICANT: Glasgow, Benjamin J. TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS FILE REPERENCE: 22000-20596.00
| CURRENT APPLICATION NUMBER: US/09/110,716A
| CURRENT FILING DATE: 1998-07-07
| CURRENT FILING DATE: 1998-07-07
| SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                         41.0%; Score 43; DB 10; Length 74; 64.3%; Pred. No. 1.3; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hawkins, Phillip R.
TITLE OF INVENTION: BREAST TUMOR SPECIFIC PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Akerblom, Ingrid E. Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 8, Application US/09934054
; Patent No. US20020107385A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murry, Lynn E.
Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RELEELNVPGEIVE 14
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                                                                                                                                                                                                                                                                                                                                                        ORGANISM: PrC2
                                                                                                                                                                                                                                                                                                                                                                             US-09-110-716-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-934-054-8
                                                                                                                                                                                                                                                                                         SEQ ID NO 38
                                                                                                                                                                                                                                                                                                              LENGTH: 74
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Gaps
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                                                                          41.0%; Score 43; DB 10; Length 2492;
40.9%; Pred. No. 82;
Live 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Adminious, Nobel 1.

APPLICANT: XU, H Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA, 011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-23

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-11-22

PRIOR PELING DATE: 2000-11-22

PRIOR FILING DATE: 2000-11-22

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-12-16

PRIOR FILING DATE: 2001-12-16

PRIOR FILING DATE: 2001-12-16

PRIOR FILING DATE: 2001-12-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
40.0%; Score 42; DB 10; Length 304;
Best Local Similarity 41.2%; Pred. No. 10;
Matches 7; Conservative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                   Sequence 14025, Application US/09815242
Patent No. US20020061569Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5720, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                      Db 1174 EKLSVPGKMVDWLSDRPEATFR 1195
                                                                                                                                                              4 EELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIZOGUCHI, HIROSHI
                                                              Query Match
Best Local Similarity 40.99
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAYSHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 PGEIVEXLXXXEESITR 25
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                                                                                                                                                                                                                                                                                                US-09-815-242-14025
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US-09-738-626-5720
                        US-09-991-258-3
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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Patent No. US20020141975A1

GENERAL INFORMATION

APPLICANT: Clasted, Robert

APPLICANT: Reith, Paula

APPLICANT: Maughan, Maureen

APPLICANT: Maughan, Maureen

APPLICANT: Maughan, Maureen

APPLICANT: Swanstron, Robert

APPLICANT: Swanstron, Robert

APPLICANT: Swanstron, Robert

APPLICANT: Maughan, APPLICANT: Old 13.000103

TITLE OF INVENTION: ALPHAYIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE

FILE REFERENCE: 01113.000103

CURRENT APPLICATION NUMBER: US/09/991,258

FILOR APPLICATION NUMBER: 09/902,537

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-07-09

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975Ale = OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                 COUNTY: USA
ZIP: 94025-6936
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/934,054
FILING DATE: 21-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.0%; Score 43; DB 10; Length 112; 64.3%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION UNBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0077 US
TELEPONNUNICATION INFORMATION:
TELEPONS: (650) 845-0166
INFORMATION FOR SEQ ID NO: 81
SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/747,547
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECUIE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-934-054-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 112 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RELEELNVPGEIVE 14
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US-09-991-258-3
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TITLE OF INVENTION: No. US20030023075Alel Sequences of E. coll 0157 NUMBER OF SEQUENCES: 265
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                                                                Gaps
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COMPUTER READBLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage COMPUTER: IDM COMPALIDE COMPATION TYPE: Diskette, 3.50 inch. 1.44Mb storage COMPUTER: Diskette, 8.00 COMPUTER: Word Perfect 8.00 CURRENT APPLICATION NATA: 8.00 FILING DATE: 01-Apr.2002

CLIRENT APPLICATION NAMER: 05/10/114,170

FILING DATE: 01-Apr.2002

FILING DATE: 03-DEC-1999

FILING DATE: 03-DEC-1999

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-1998

ATTORIEST/AGENT IRFORMATION:

ATTORIEST/AGENT INFORMATION:

ATTORIEST/AGENT INFORMATION:
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                    38.1%; Score 40; DB 10; Length 360; 54.5%; Pred. No. 27;
                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-10-114-170-265
                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 4814, Application US/09738626
                                                                                                                                                                                                                                                                Sequence 265, Application US/10114170

Publication No. US20030023075A1

GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                            Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 RSLVEVSIPGELLTDFRQIQNNV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 519 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RELEELNVPGEIVEXLXXXEESI 23
                                                                                                                                                                                                                                                                                                                                                 Burland, .-. Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (608) 251-916
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      Plunkett, Guy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                  Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
                                                                                                                   3 LEELNVPGEIV 13
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73 VEEFNVPGSVI 83
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US-09-361-741-4
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Best Local Similarity 47.4%; Pred. No. 14;
Matches 9; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, ADDRESSEE: STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD CITY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION, PETER L
APPLICANT: HUDSON, PETER L
APPLICANT: HE, WEI WE
TITLE OF INVENTION: PROSTATIC GROWTH FACTOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                       TITLE OF INVENTION: NOVELS OF THE REPERBNCE: 249-125
FILE REPERBNCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PRILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR PLILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER: OF SEQ ID NOS: 7059
SEQ ID NO 5720
LENGTH: 275
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                APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,741
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Corynebacterium glutamicum US-09-738-626-5720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/411,607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIONALIA PERRARO, GREGORY D
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 3258C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)994-174
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 mmino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09361741
Patent No. US20020048784A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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196 DVPAEIIEKERSIAEQITR 214
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TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07068
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37.1%; Score 39; DB 9; Length 1248;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.2%; Score 38; DB 10; Length 421; Conservative 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                 FILE REFERENCE: 249-125
CURRENT APPLICATION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/99/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VOICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09767770A
Sequence 4, Application US/09767770A
GENERAL INFORMATION:
APPLICANT: Michalovich David
APPLICANT: Sims, Matthew Alan
APPLICANT: Sims, Matthew Alan
APPLICANT: Sims, Matthew Alan
APPLICANT: Shalkh, Narjis
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30086-C1
CURRENT FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 080622.7
PRIOR APPLICATION NUMBER: 982029.7
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
LENGTH: 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Corynebacterium glutamicum US-09-738-626-4814
                                       APPLICANT: NNKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: YOKOI, HAKUHIKO
APPLICANT: YOKOI, HAKUHIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEBA, MASATO
Publication No. US20020197605A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                            OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: HOMO SAPIENS
US-09-767-770A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
'.has 6; Conserve
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Publication No. US20020194645A1
GENERAL INFORMATION.
APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEG ID NOS: 61
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TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE
TITLE REFERENCE: 0342/16548-0329
CURRENT APPLICATION NUMBER: US/20/893,519A
CURRENT FILING DATE: 2001-06-28
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-06-29
NUMBER OF SEQ ID NOS: 146
SSCTWARE: PATENTIN NOS: 146
SSCTWARE: PATENTIN VEFSION 3.1
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36.2%; Score 38; DB 9; Length 611
Best Local Similarity 37.5%; Pred. No. 1.1e+02;
Matches 6; Conservative 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
NAME/KEY:
OTHER INFORMATION: Corresponds to SEQ ID NO: 101
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Human Genbank/NP_001078
BLATABASE ENTRY DATE: 2001-12-18
RELEVANT ESIDUES: (1)..(611)
                                                                                           APPLICANT: ANADYS PHREMACEUTICALS, INC.
APPLICANT: THOMPSON, Craig
APPLICANT: MOORE, Jeffrey
APPLICANT: BUCKAN, Ed T.
APPLICANT: BRADLEY, John
APPLICANT: DESILVA, Thamara
APPLICANT: DESILVA, Thamara
APPLICANT: KOMARNITSKY, Svetlana
APPLICANT: MOORE, Daniel
APPLICANT: MOORE, Daniel
APPLICANT: MOCRE, Daniel
                          ; Sequence 28, Application US/09893519A; Publication No. US20030027243A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         SANDERSON, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|::|| :| :::| |
592 QEVQELPIPSKLLEFL 607
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SEQ ID NO 40
LENGTH: 173
                                                                                                                                                                                                                                                                                                                                                                                                HAQ, Tariq
ZHU, Shuhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LONG,
US-09-893-519A-28
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LENGTH: 611
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US-09-853-450-40
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GENERAL INFORMATION:
APPLICANT: Hu, Jing-Shan
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Polynucelotides Encoding Vascular Endothelial Growth
TITLE OF INVENTION: Polynucelotides
CURRENT APPLICATION NUMBER: US/09/618,451
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-03-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
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US-09-853-450-50
Sequence 50, Application US/09853450
Sequence 50, Application No. US202020194645A1
Spublication No. US202020194645A1
Spublication No. US202020194645A1
Spublicatur Peace Spublication No. US202020194645A1
SAPPLICANT: Polta, Gary
APPLICANT: Polta, Gary
APPLICANT: Polta, Gary
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
FILE REFERENCE: 19452A-002400US
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.1
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                                                                                                            Query Match 35.2%; Score 37; DB 9; Length 173; Best Local Similarity 40.9%; Pred. No. 37; Matches 9; Conservative 3; Mismatches 10; Indels
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; Publication No. US20020182683A1
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                                                                                                                                                                                                                                               :||| || || : | || : | 103 KLEEPNVDNVSVDSLISLEEQL 124
                                                                                                                                                                                                                   2 ELEELNVPGEIVEXLXXXEESI 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana
ORGANISM: Arabidopsis thaliana
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                                                   ; OTHER INFORMATION: AGL27 US-09-853-450-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-060-523-7
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35.2%; Score 37; DB 9; Length 196; 35.3%; Pred. No. 43; Tindels tive 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYBE: Floppy disk
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC Compatible
COMPREM: DATEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.30
CURRBW APPLICATION DATA:
APPLICATION NUMBER: US/10/084,488
                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hu, Jin-Shan
APPLICANT: Craig, Rosen
APPLICANT: Cao, Liang
TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
FILE REFERENCE: PF112P3D1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/623,725
FILING DATE: 07-Sep-2000
APPLICATION NUMBER: US 09/042,105
FILING DATE: 13-MAR-1998
APPLICATION NUMBER: US 09/107,997
FILING DATE: 30-JUN-1998
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/935,726
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 09/438,538
PRIOR FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 28-Feb-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          35.2%;
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 EELNVPGEIVEXLXXXE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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              35.2%
Query Match
Best Local Similarity 35.3%
Matches 6; Conservative
                                                                            4 EELNVPGEIVEXLXXXE 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-084-488-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                  196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                RESULT 14
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(without alignments)
93.903 Million cell updates/sec
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| cgn2_6/ptodata/1/paa/Pc0.COMB.pep:*
| cgn2_6/ptodata/1/paa/US06_COMB.pep:*
| cgn2_6/ptodata/1/paa/US08_COMB.pep:*
| cgn2_6/ptodata/1/paa/US09_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4569144
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4569144 seqs, 644733110 residues
                                                                                                                                                                                                                                                                                                                                                                                                                        1 RELEBLINVPGEIVEXLXXXEESITR 25
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Listing first 45 summaries
                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description								
SUMMARIES		ID	115-08-621-564-2		10 US-08-621-564A-2	US-09-222-791-2	HS-08-666-559-33	70 00 - 666 - 550 - 23	0.5-00-00-50 (US-09-380-/38A-2
		Query Match Length DB		OT C7	25 10	25 16	48 10	0 0	209 TO	25 17
	ф	Query Match	1 0	7.96	96.3	0 9 0		70.5	96.2	A CO
		Score	111111	101	101	101	107	TOT	101	07
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Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 103, Appl Sequence 35, Appl Sequence 35, Appl Sequence 34394, A Sequence 141484,	aquence 33, equence 31, equence 31, equence 38, equence 8, equence 92, equence 92, equence 92, equence 180, equence 200, equence 200, equence 3, equence 8, equence 8	Sequence 152, App Sequence 152, App Sequence 15290, A Sequence 15290, A Sequence 2147, App Sequence 14025, A Sequence 1625, A Sequence 1625, A Sequence 1625, A Sequence 1625, A Sequence 1621, A Sequence 162
S-07-731-592B-2 US-08-621-564-1 US-08-661-564A-1 US-08-666-559-103 US-08-666-559-35 US-10-219-999-52212 US-09-708-427-34394 US-09-701-537-141484	us. 10-791-537-14140 us. 10-219-999-33152 us. 60-324-109-17126 us. 60-324-109-17156 us. 60-110-716-38 us. 60-110-716-38 us. 60-9747-547-8 us. 60-999-33353 us. 60-999-33353 us. 60-999-33533 us. 60-999-33533 us. 60-999-33533 us. 60-9999-33533 us. 60-9999-33533 us. 60-9999-33533 us. 60-9999-33533 us. 60-991-253-691-394 us. 60-991-253-39 us. 60-991-258-39 us. 60-991-258-39 us. 60-991-258-39	US-09-791-537-61885 US-09-882-227-152 US-09-882-227-152 US-00-096-409-15290 US-60-1079-131-8159 US-60-161-932-2147 PCT-USO1-08631-32346 PCT-USO2-03987-14025 US-09-815-242-14025 US-10-072-851-14025 US-10-072-851-14025 US-09-902-540-10621
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7 8 8 10 11 112	116 116 117 118 118 118 118 118 118 118 118 118	% % % % % % % % % % % % % % % % % % %

ALIGNMENTS

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RESULT 1
Sequence 2, Application US/08621564
Sequence 3, Application US/08621564
APPLICANT: Han, Sang Kee
APPLICANT: Shin, Yoo Cheol
APPLICANT: Shin, Yoo Cheol
APPLICANT: Shin, Yoo Cheol
APPLICANT: Shin, Yoo Cheol
TITLE OF INVENTION: SAME, AND PROCESS FOR THE PREPARATION THEREOF
TITLE OF INVENTION: SAME, AND PROCESS FOR THE PREPARATION THEREOF
TITLE OF INVENTION: SAME, AND PROCESS FOR THE PREPARATION THEREOF
TITLE OF INVENTION: SAME, AND PROCESS FOR THE PREPARATION THEREOF
COUNTRY: Alexandria
STRATE: VA
COUNTRY: USA
ZIP: 22314
STATE: VA
COUNTRY: IBM PC-DOS/NS-DOS
OPERATIOS SYSTEM: PC-DOS/NS-DOS
OPERATIOS SYSTEM: PC-DOS/NS-DOS
OPERATION NUMBER: US/08/621,564
FILING DATE:
APPLICATION NUMBER: US/08/621,564
FILING DATE:
CLASSIFICATION NUMBER: 36,190
REGISTRATION NUMBER: 2438-022
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                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HAN, Sang Kee
APPLICANT: SHIN, YOO Cheol
TITLE OF INVENTION: SAME AND PROCESS FOR THE PREPARATION THEREOF
INVERSED OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
                                                                                                                                                                                                96.2%; Score 101; DB 10; Length 25;
84.0%; Pred. No. 5.5e-10;
tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.2%; Score 101; DB 10; Length 25; 84.0%; Pred. No. 5.5e-10; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,564A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29,310
RER: 2438-022
                                                                                                                                                                                                                                                          1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 684-1111
TELEFAX: (703) 684-1124
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 124
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Hauptman, Benjamin J.
REGISTRATION NUMBER: 29,310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-1996
N: 530
                                                                                                                                                                                                                                Conservative
                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-621-564-2
                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alexandria : Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                STRANDEDNESS:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 22314
                                                                                                                                                                                                                                                                                                                                                    US-08-621-564A-2
                                                                                                                                                                                                                              21;
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US-09-222-791-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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APPLICANT: Chen, Wen-Yih
APPLICANT: Chen, Wen-Yih
APPLICANT: Huang, Shih-Yow
APPLICANT: Huang, Shih-Yow
APPLICANT: Huang, Shih-Yow
APPLICANT: Lin, Fu-Yong
TITLE OF INVENTION: Caselnophosphopeptides from Caseln Hydrolysate by Using
TITLE OF INVENTION: an Immobilized Metal Ion Affinity Chromatography
CURRENT APPLICANION NUMBER: US/09/222,791
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                               96.2%; Score 101; DB 16; Length 25; 84.0%; Pred. No. 5.5e-10; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jean-Marc CHOBERT et al.
TITLE OF INVENTION: METHOD FOR PREPARING PEPTIDE
TITLE OF INVENTION: PRODUCTS, AND RESULTING PRODUCTS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/OB/666,559
FILING DATE: September 10, 1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: FR 93 15764
FILING DATE: December 23, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09222791 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
N-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application US/08666559; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P14764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P1470
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 716-1191
TELEFAX: (703) 716-1191
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 diskette
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                     21; Conservative
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                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Bos taurus
US-09-222-791-2
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arnold Turk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: no
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FRAGMENT TYPE:
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US-08-666-559-33
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                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                         SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                              LENGTH:
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Matches
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ADDRESSEE: Patent Department, Unllever United States, Inc. STREET: 45 River Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-translationally phosphorylated serine
                                                                                                                                                                                                                                                                                                                                                                                          Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Burger, Allan R.
APPLICANT: Bliott, David L.
APPLICANT: Schick, Laura A.
APPLICANT: Schick, Laura A.
TITLE OF INVENTION: Oral Compositions Containing
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 92.4%; Score 97; DB 17; 1
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                           COCATION: (15)...(15)
OTHER INFORMATION: Xaa is a phosphorylated Serine NAME/KEY: miso_feature
LOCATION: (17)...(17)
OTHER INFORMATION: Xaa is a phosphorylated Serine
                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (18)..(18)
OTHER INFORMATION: Xaa is a phosphorylated Serine
                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (19)..(19)
OTHER INFORMATION: Xaa is a phosphorylated Serine
US-09-380-738A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/07/731,592B
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US-07-31-592B-2
US-07-31-592B-2
Sequence 2, Application US/07731592B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word(R)
CURRENT APPLICATION DATA:
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16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Phosphoserine
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1991071
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Unknown
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OPERATING SYSTEM:
                                                                                                                                                   NAME/KEY: misc_feature
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                                                                                                                  ORGANISM: Bos sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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0
                                               4; Indels
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APPLICANT: REPRINCIDS, CALCIUM PHOSPHOPEPTIDE COMPLEXES
FILE REPERENCE: 040268/016.
GURRENT APPLICATION NUMBER: US/09/380,738A
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/AU98/00160
PRIOR APPLICATION NUMBER: AU POS662
                                                                                                                                                                                                                                  APPLICANT: Jean-Marc CHOBERT et al.
TITLE OF INVENTION: METHOD FOR PREPARING PEPTIDE
TITLE OF INVENTION: PRODUCTS, AND RESULTING PRODUCTS
CORRESPONDENCES: 122
CORRESPONDENCE ADDRESS:
                           84.0%; Pred. No. 1.4e-09;
tive 0; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Greenblum & Bernstein, P.L.C. STREET: 1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER. MS-DOS
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1+ (ASCII)
SOFTWARE: WORD PERFECT 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,559
FILING DATE: September 10, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14764
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 716-1191
TELEFAX: (703) 716-1191
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/09380738A; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: FR 93 15764
APPLICATION NUMBER: FR 93 15764
FILING DATE: December 23, 1993
ATTORNEY/AGENT INFORMATION:
NAME: ARROLIG TURK
                                                                                                                                                                                                                Sequence 23, Application US/08666559
GENERAL INFORMATION:
                                                                                        1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                              MEDIUM TYPE: 1.44 www.mediuple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.44 diskette
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                                     Best Local Similarity 84.09 Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                         RESULT 5
US-08-666-559-23
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GENERAL INFORMATION:
APPLICANT: Han, Sang Kee
TITLE OF INVENTION: CASEIN PHOSPHOPEPTIDE, CASEIN CONTAINING
TITLE OF INVENTION: SAME, AND PROCESS FOR THE PREPARATION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                           OTHER INFORMATION: POSt-translationally phosphorylated OTHER INFORMATION: serine
                                                                                                                Post-translationally phosphorylated serine
                                                                                                                                                                        91.4%; Score 96; DB 3; Length 24;
83.3%; Pred. No. 3.9e.09;
tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.4%; Score 96; DB 10; Length 28;
83.3%; Pred. No. 4.8e-09;
tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
COFFWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/621,564
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF LINEAR OF SEQUENCES: 7
NUMBER OF SEQUENCES: 7
OCRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, Price, Leblanc & Becker
STREET: 99 Canal Center Plaza, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2438-022
                                                                                                                                                                                                                               2 ELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                   CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 2438-
TELECOMMUNICATION:
TELEPHONE: (703) 684-1111
TELEFAX: (703) 684-1124
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RELEELNVPGEIVEXLXXXEESIT 24
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                                                                              Phosphoserine
                                                                                                                                                                            Best Local Similarity 83.38
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                      COCATION: 18 CTHER INFORMATION: CTHER INFORMATION: US-07-731-592B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear

// MOLECULE TYPE: protein

US-08-621-564-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
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Best Local Similarity
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                                                        FEATURE:
NAME/KEY:
NAME/KEY:
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               LOCATION:
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                                                                                                                                                                     Query Match
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US-08-621-564A-1

RESULT 9

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APPLICANT: HAN, Sang Ree
APPLICANT: HAN, Sang Ree
APPLICANT: SHIN, Yoo Cheol
TITLE OF INVENTION: CASEIN PHOSPHOPEPTIDE, CASEIN CONTAINING
TITLE OF INVENTION: SAME AND PROCESS FOR THE PREPARATION THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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91.4%; Score 96; DB 10; Length 28;
Best Local Similarity 83.3%; Pred. No. 4.8e-09;
Matches 20; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 103, Application US/08666559
GENERAL INFORMATION:
APPLICANT: Jean-Warc CHOBERT et al.
TITLE OF INVENTION: METHOD FOR PREPARING PEPTIDE
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATE: DS. NAS-DOS CURRENT APPLICATION DATA: PELCHIC Release #1.0, Version #1.30 PPLICATION NUMBER: US/08/621 F. CLASSIFFT.
                                                                                                                                                  ADDRESSEE: LOWE PRICE LEBLANC & BECKER STREET: 99 Canal Center Plaza, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Greenblum & Bernstein, P.L.C. STREET: 1941 Roland Clarke Place CITY: Reston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,310
REFERENCE/DOCKET NUMBER: 2438-022
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
; Sequence 1, Application US/08621564A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/66,559
FILING DATE: September 10, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RELEELNVPGEIVEXLXXXEESIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hauptman, Benjamin J. REGISTRATION NUMBER: 29,31(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703-684-1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 703-00: TELEPHONE: 703-684-1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 dis
                                                                                                                                                                                      CITY: Alexandria
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: USA
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                                                                                                                                                                                                             STATE:
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Best Local Similarity
                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.4%; Score 55; DB 10; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHOD FOR PREPARING PEPTIDE TITLE OF INVENTION: PRODUCTS, AND RESULTING PRODUCTS NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,559
FILING DATE: September 10, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14764
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FR 93 15764 FILING DATE: December 23, 1993 ATTORNEY/AGENT INFORMATION:
                                                                              ATIONEL ASTOOD TURK
REGISTRATION NUMBER: 33,094
REGISTRATION NUMBER: P14764
TELECOMMUNICATION INFORMATION:
TELEPRAN: (703) 716-1191
TELEPRAN: (703) 716-1190
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jean-Marc CHOBERT et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35, Application US/08666559
GENERAL INFORMATION:
                     APPLICATION NUMBER: FR 93 15764
                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ELEELNVPGEIVEXLXXXEESITR 25
                                           FILING DATE: December 23, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ELEELNVPGEIVESL-SSEESITR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 716-1191
TELEFAX: (703) 716-1191
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .44 diskette
                                                                                                                                                                                                                            LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arnold Turk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Virginia
COUNTRY: U.S.A.
ZIP: 20191
                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-666-559-35
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                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Query Match

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Sequence 34394, Application US/09708427

Sequence 34394, Application US/09708427

GENERAL INFORMATION:
GENERAL INFORMATION:
THE REPRESSION:
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 34394
LENGTH: 334
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                                                       APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Edgerton, Michael D
APPLICANT: Biderton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stein, Joshua
CURRENT STEIN, DATE: 2002-08-15
CURRENT APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-15
PRIOR FILING DATE: 2001-09-15
NUMBER: OF SEQ ID NOS: 63520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.6%; Score 51; DB 26; Length 321;
44.0%; Pred. No. 9.8;
tive 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..334
OTHER INFORMATION: Ceres Seq. ID 1838367
US-09-708-427-34394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RELEELNVPGEIVEXLXXX--EESITR 25
RESULT 12
US-10-219-999-52212
; Sequence 52212, Application US/10219999
; GENERAL INFORMATION: ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 RELQLINMRKEMVQYLQTGQESIAR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 37.08
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
US-10-219-999-52212
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 52212
LENGTH: 321
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32 KEFEKIHIPNEIVEEILVRLPVKSLTR 58

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APPLICANT: Debe, Daries, Darie
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GENERAL INFORMATION:
APPLICANT: Bloomix, Inc.
APPLICANT: Dancer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: MINDER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
CURRENT FILING DATE: 2001-02-22
SOFTWARE: PATENTING VERSION 3.0
SEQ ID NO 141465
LENGHTH 492
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Best Local Similarity 61.5%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 42.9%; Score 45; DB 21; Length 492; Best Local Similarity 61.5%; Pred. No. 2e+02; Matches 8; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Methanobacterium thermoautotrophicum US-09-791-537-141484
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US-09-791-537-141484; Sequence 141484, Application US/09791537; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: February 11, 2003, 18:33:21 Job time : 172.649 secs
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201 KELNVPGDAIEKL 213
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205 KELNVPGDAIEKL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 EELNVPGEIVEXL 16
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APPLICANT: Mitcham, Jennifer
APPLICANT: Skelky, Yasir
APPLICANT: Persing, David
APPLICANT: Bhatia, Alay
APPLICANT: Maisonneuve, Jean Francois
APPLICANT: Zhang, Yanni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang, Siqing
Jen, Shyian
                                                                                                                                                                                                                                                                                                        US-09-857-346-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEO ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                           RESULT 1
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Sequence 7957, Ap
Sequence 7957, Ap
Sequence 5858, Ap
Sequence 7281, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Appl
Sequence 22619, A
Sequence 22619, A
Sequence 4794, Ap
Sequence 4, Appli
Sequence 5460, Ap
Sequence 68459, A
Sequence 68459, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5016, Ap
Sequence 15497, A
Sequence 15497, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        App
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Sequence 4, Appli
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Sequence 3, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Ap
Sequence 294,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28,
                                                                                           (without alignments)
72.734 Million cell updates/sec
                                                                        February 11, 2003, 18:17:56 ; Search time 28.6082 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
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                                                                                                                                                                                                                                                                                                                                                                  Pending_Patents_AA_New:*

1. /cgn2_6/ptodata/2/paa/pcr_NEW_COMB.pep:*

2. /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3. /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

4. /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

5. /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7. /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7. /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7. /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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US-10-057-498-22619
US-10-057-498-22619
US-10-057-498-22619
US-10-077-4
US-09-950-084-5460
US-09-950-084-5460
US-09-950-084-5460
US-09-950-084-5460
US-09-957-1546-29
US-10-092-411A-5016
PCT-USO2-3277-15497
US-10-057-488-15497
US-10-259-453-3
US-09-949-002-294
US-09-949-002-485
US-10-315-898-9519
US-10-315-898-9557
US-10-510-67-79557
US-10-510-67-79557
US-10-510-67-79557
US-09-959-0084-5958
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                           1 RELEELINVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                          420401 seqs, 83231269 residues
                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                      US-09-380-738A-2
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                                                                                        Run on:
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1;
                                                              Sequence 26, Appli
Sequence 5503, Appli
Sequence 5503, Appli
Sequence 61152, A
Sequence 61152, A
Sequence 61153, A
Sequence 61153, A
Sequence 5439, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 1841, Appli
                       40, Appl
61154, A
61154, A
50, Appl
Sequence 29941, A
        Sequence 3821, Ap
Sequence 3821, Ap
                                         Sequence 611
Sequence 50,
Sequence 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                          Sequence
                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        39.0%; Score 41; DB 5; Length 196; 40.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
3; Mismatches
                                                                                                                                                                                                                                     APPLICANT Burn, Joanne E
APPLICANT Burn, Joanne E
APPLICANT PRESCOCK, William J.
APPLICANT Dennis, Blizabeth S
APPLICANT Bennis, Blizabeth S
APPLICANT Belliwell, Candice C
APPLICANT ROUSE, Dean T
TITLE OF INVENTION: Control of Flowering
FILE REFERRNCE: 050341-0041
CURRENT APPLICATION WUMBER: US/09/857,346
CURRENT APPLICATION NUMBER: PP 7469
PRIOR APPLICATION NUMBER: PP 7469
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR PILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 42
SOFTWARR: Patentin Version 3.1
                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ELEELNVPGEIVEXLXXXEE----SITR 25
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                                                                                                                                                                                                                       ; sequence 27, Application US/09857346; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
       148
1161
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Matches 12; Conserv
        US-09-857-346-27
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         337
728
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748
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768
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778
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Lodes, Michael

APPLICANT:

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APPLICANT: George H. Miller
APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
APPLICANT: Karen J. Shaw
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
CURRENT APPLICATION NUMBER: US/09/950,084
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US 09/417,811
                                                                                                                                                                                                                  Gaps
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                                                                                                                            39.0%; Score 41; DB 6; Length 1037; 28.0%; Pred. No. 2.1e+02; tive 10; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hudson, et al.
TITLE OF INVENTION: Prostatic Growth Factor FILE REFERRNGE: PF149D2
CURRENT APPLICATION NUMBER: US/10/270,377
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 09/361,741
PRIOR FILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,555
PRIOR PILING DATE: 1999-03-11
PRIOR PELING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR PILING DATE: 1999-03-11
PRIOR PILING DATE: 1999-03-11
PRIOR PILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,541
PRIOR APPLICATION NUMBER: US 09/267,934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/461,418
PRIOR FILING DATE: 1999-11-18
PRIOR PILING DATE: 1995-11-18
PRIOR PILING DATE: 1995-04-11
PRIOR PILING DATE: 1995-04-11
PRIOR APPLICATION NUMBER: 08/4/14578
PRIOR FILING DATE: 1994-12-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VETSION 3.1
LENGTH: 360
                    ; ORGANISM: Staphylococcus epidermidis US-10-092-411A-4794
                                                                                                                                                                                                                                                                                       | ::|:: |:| |:| |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| 
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PRIOR APPLICATION NUMBER: US 09/353,718
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR PRICIATION NUMBER: US 09/266,557
PRIOR PRICIATION NUMBER: US 09/266,556
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GENERAL INFORMATION: APPLICANT: George H. Shimer, Jr.
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                                                                                      Ouery Match
Best Local Similarity 28.00,
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Best Local Similarity 54.59
Warches 6; Conservative
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US-10-270-377-4
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DATE: 2002-03-07
CURRENT APPLICATION NUMBER: US/10/092,411A
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5676

LENGTH: 1037

"LENGTH: 1037
                                                                               APPLICANT: Barth, Brenda
APPLICANT: Barth, Brenda
APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes of TITLE REPERENCE: 210121, 514c1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT PILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 22619
LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.51,
CURRENT APPLICATION NUMBER: US/10/057,498
NUMBER OF SEQ ID NOS: 29212
SEQ ID NO 22219
LENGTH: 221
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88.9%; Pred. No. 31;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.0%; Score 41; DB 6; Length 221; 88.9%; Pred. No. 31; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 22619, Application US/10057498; GENERAL INFORMATION: APPLICANT: Mitcham, Jennifer
                                                                 Carter, Darrick
Barth, Brenda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
Benson, Darin
Jones, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Propioni acnes
PCT-US02-32727-22619
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Matches 8; Conserv
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Matches 8; Conserved
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APPLICANT:
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36.2%; Score 38; DB 5; Length 196;
Best Local Similarity 40.9%; Pred. No. 84;
Matches 9; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.2%; Score 38; DB 5; Length 82; 50.0%; Pred. No. 28; tive 4; Mismatches 3; Indels
                                                                                                                                                                                                                  APPLICANT: Compugen LTD
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION VUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOGTWARE: Patentin version 3.2
SOGTWARE: Patentin version 3.2
EROGTH: 82
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Sequence 28, Application US/09857346
Sequence 28, Application US/09857346
Sequence 28, Application US/09857346
Sequence 28 Application US/09857346
APPLICANT: Bearcock, William J.
APPLICANT: Palliwell, Candice C.
APPLICANT: Helliwell, Candice C.
APPLICANT: Helliwell, Candice C.
APPLICANT: Rouse, Dean T.
TITLE CF INVENTION: Control of Flowering
TITLE REFERENCE: 05034-0041
CURRENT FILING DATE: 1998-12-03
PRIOR FILING DATE: 1998-10-22
PRIOR FILING DATE: 1998-10-22
PRIOR PILING DATE: 1999-11-22
PRIOR PILING DATE: 1999-11-22
PRIOR PILING DATE: 1999-11-22
PRIOR FILING DATE: 1999-11-22
PRIOR FILING DATE: 1999-11-22
SOFTWARE: PETCATION NUMBER: US GO/116,928
PRIOR FILING DATE: 1999-11-22
SOFTWARE: PETCATION NUMBER: US GO/116,928
PRIOR FILING DATE: 1999-11-22
SOFTWARE: PETCATION NUMBER: US GO/116,928
PRIOR FILING DATE: 1999-11-20
SOFTWARE: PETCATION NUMBER: US GO/116,928
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                                                                                                                                                                             ; Sequence 68459, Application US/09724676A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 KLEESNVDNVSVDSLISMEEQL 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 50.0 tes 7; Conservative
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34 RGLQETDVPGALVD 47
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US-09-724-676A-68459
                  1 RELEELNVPGEIVE 14
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US-10-092-411A-5016
                                                                                                                                                RESULT 9
US-09-724-676A-68459
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APPLICANT: Ferguson, K.
APPLICANT: Homberger, S.
APPLICANT: Homberger, S.
TITLE OF INVENTION: ANIMAL MODELS AND METHODS FOR ANALYSIS OF LIPID METABOLISM AND STITLE OF INVENTION: OF PHARMACEUTICAL AND PESTICIDAL AGENTS THAT MODULATE LIPID METAFILE REPERENCE: 7226-101, ESS9-004
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PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: US 09/036,720
PRIOR FILING DATE: 1998-03-06
PRIOR REDIGATION NUMBER: US 09/036,338
PRIOR FILING DATE: 1998-03-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 7451
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                                                                                                                                                                                                                                                                                                                            Ouery Match 37.1%; Score 39; DB 5; Length 1067; Best Local Similarity 29.2%; Pred. No. 4.8e+02; Matches 7; Mismatches 10; Indels Matches
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 1291B1.4 Compugen
FILE REFERENCE: 1291B1.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
LENGTH: 82
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CURRENT FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 68459, Application US/09724676
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 8, Application US/09332522E
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               955 ELEHMNMEDDGFYQVPGEVLE 975
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                                                                                                                                                                                                                                                                  , ORGANISM: Staphylococcus aureus US-09-950-084-5460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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SEQ ID NO 5460
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acr FILE REPERENCE: 210121.314
CURRENT APPLICATION NUMBER: US/10/057,498
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 29212
LENGTH: 701
                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-15497
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Best Local Similarity
The 6; Conserva
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LENGTH: 754
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LENGTH: 833
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/10/092,411A PRIOR TILING DATE: 2002-03-07 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1998-08-13 PRIOR FILING DATE: 1998-08-13 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-08-14 NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 PRIOR FILING DATE: 1997-08-14 PRIOR PRIOR FILING DATE: 1997-08-14
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APPLICANT: Douglass.John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514C1
                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                         Query Match 36.2%; Score 38; DB 6; Length 270; Best Local Similarity 53.8%; Pred. No. 1.3e+02; Matches 7; Conservative 2; Mismatches 4; Indels
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31.6%; Pred. No. 4.2e+02;
tive 7; Mismatches 6; Indels
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CURRENT FILING DATE: 2002-10-11
SEQ ID NO 15497
LENGTH: 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 15497, Application PC/TUS0232727; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Persing, David
Bhatia, Ajay
Malsonneuve, Jean Francois
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GRNERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
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APPLICANT: Skeiky vasir
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Jen, Shyian
Lodes, Michael
Benson, Darin
Jones, Robert
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Barth, Brenda
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Matches 6; Conservative
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ORGANISM: Propioni acnes
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LENGTH: 270
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APPLICANT:
APPLICANT:
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APPLICANT:
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36.2%; Score 38; DB 6; Length 701; 31.6%; Pred. No. 4.2e+02; tive 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.2%; Score 38; DB 6; Length 754; 30.0%; Pred. No. 4.6e+02; tive 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                        US-10-259-453-4

Sequence 4, Application US/10259453

Sequence 4, Application US/10259453

SEQUENCEAL INFORMATION

APPLICANT: COMPUGEN LTD

APPLICANT: APPLICANT: LEVINE, Zurit

APPLICANT: BERNSTEIN, Jeanne

APPLICANT: SAVITZEK, Kinneret

TITLE OF INVENTION: P13K-REGULATORY SUBUNIT HOMOLOGY

CURRENT APPLICATION NUMBER: US/10/259,453

CURRENT APPLICATION NUMBER: US/10/259,453

PRIOR APPLICATION NUMBER: IL 135310

PRIOR APPLICATION NUMBER: IL 135310

PRIOR PILING DATE: 2000-03-28

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: AZAR, Idit
APPLICANT: LEVINE, Zurit
APPLICANT: BERNSTEIN, Jeanne
TTLE OF INVENTION: P13K-REGULATORY SUBUNIT HOMOLOGY
CURRENT APPLICATION NUMBER: US/10/259,453
CURRENT APPLICATION NUMBER: L135310
PRIOR APPLICATION NUMBER: L135310
PRIOR APPLICATION NUMBER: L135310
PRIOR APPLICATION NUMBER: L135310
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENT VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 3, Application US/10259453 ; GENERAL INFORMATION:
                                                                                                                                      483 DISGHLIQRVHRHEEAITR 501
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126 EMAVPGTLYQRMVIAEQNLT 145
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                                                       6; Conservative
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US-10-259-453-3

Query Match

Query Match

Best Local Similarity 30.0%; Pred. No. 5.2e+02;

Batches 6; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 5 ELNVPGEIVEXLXXXEESIT 24

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Db 2.05 EMAVPGTLYQRMVIAEQNLT 224

Search completed: February 11, 2003, 18:35:19

Job time : 30.6082 secs
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments)
109.706 Million cell updates/sec February 11, 2003, 18:14:11; Search time 21.9072 Seconds Run on:

1 RELEELNVPGEIVEXLXXXEESITR 25 US-09-380-738A-2 Perfect score: Title:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

Sequence:

283224 seqs, 96134422 residues Searched: Total number of hits satisfying chosen parameters:

Maximum DB seg length: 200000000 Minimum DB seq length: 0

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

PIR_73:* Database :

pir1:* pir2:* pir3:* pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description								hypothetical prote	beta-casein precur	hypothetical proce	probable histiayi-			hypothetical prote	hypothetical prote	prostatic steroid-	probable glutamate	starch phosphoryla	probable ribonucle	ponetructural poly	handthatical prote		nypolnetical proce	4		<u> </u>	XIRF2 protein - nu	probable transcity		
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% Query Match L	96.2	0	1 0	56		4 0	טע	* <	4.3	43	7	$^{\circ}$		4.0	4.2.5	٦,	∹,	-	41.0	41.0	41.0	40.5		40.0		40.0	40.0	40.0	40.0	40.0
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DNA helicase I (EC hypothetical prote HTV-1 refromesin	probable rpik-fami hvnothetical prote	hypothetical prote	UL53 protein - hum	probable isomerase	copper-transportin	hypothetical prote	nonstructural poly	Na+/H+ antiporter	probable bacteriop
BVECAI G70472	S63739 AI0366	A85322 T05874	E95387	QQBEW2 B91124	A85969 E83719	576134	E86143	C44213	AG0688
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42 41.5	41 41	41	41	41 41	41	41	41	41	40.5
30 31	33.2	34	36	37	6 6	4 0 4 1	42	43	44 45

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A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Cross-references: GB:M55158; NID:g162804; PIDN:AAA30431.1; PID:g162805
A; Cross-references: GB:M55158; NID:g162804; PIDN:AAA30431.1; PID:g162805
A; Cross-references: GB:M55158; NID:g162804; F.; Willis, I.M.; Mackinlay, A.G.
A; Cross-reference: GB:M55158; NID:g162804; PMID:2833669
A; Accession: B29087
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A,MOLECUIE LYPE: MRNA A,ROSAGIUGES: 1-224 <STE> A,Cross-references: GB:M16645; NID:g162930; PIDN:AAA30480.1; PID:g162931 A; Status: translation not shown

A) Experimental source: A2 variant
R;Baev, A.A.; Smirnov, I.K.; Gorodetskii, S.I.
Mol. 21, 214-222, 1987
A) Hill: Biol. 21, 214-222, 1987
A) Frimary structure of bovine beta-casein cDNA.
A;Reference number: \$01860

A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-81, "H',83-224 <BAE>
A; Cross_references: EMBL:X06559; NID:g171; PIDN:CAA29658.1; PID:g757752
A; Cross_references: EMBL:X06559; NID:g171; PIDN:CAA29658.1; PID:g757752
A; Experimental source: A1 variant
A; Mote: this paper is a translation of the Russian paper published in Mol. Biol. Mo
A; Mote: this paper is a translation of the Russian paper published in Mol. Biol. Mo
A; Jimenez-Flores, R.; Kang, Y.C.; Richardson, T.
B; Jimenez-Flores, R.; Kang, Y.C.; Richardson, T.
B; Jimenez-Flores, R.; Kang, Y.C.; Richardson, T.
B; Jitle: Cloning and sequence analysis of bovine beta-casein cDNA.
A; Reference number: A25846
A; Accession: A25846
A; Molecule type: mRNA
A; Residues: 1-107, L',109-151, 'PL',154-209, 'O',211-224 <JIM>A; Cross_references: GB:MI5132; NID:g162796; PIDN:AAA30430.1; PID:g162797
A; Cross_references: GB:MI5132; NID:g162796; PIDN:AAA30430.1; PID:g162797
A; Cross_references: GB:MI5132; NID:g162796; PIDN:AAA30430.1; PID:g162797
A; Ttle: A new strategy for primary structure determination of proteins: applicatic A; Ttle: A new strategy for primary structure determination of solutions application A; Reference number: S02429; MUID:88152252; PMID:3278933

A;Molecule type: protein A;Residues: 16-81,'H',83-224 <CAR> A;Experimental source: Al variant R;Yan, S.B.; Wold, F.

Gaps

. 0

Indels

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Asterior section variant CnH - bovine
C; Species: Bos primigentus taurus (cattle)
C; Species: Bos primigentus taurus (cattle)
C; Accession: A59068; B59068
R; Han, S.K.; Shin, Y.C.
Anim. Genet. 27(Suppl.2), 91b, 1996
A; Title: Biochemical characterization of the new beta-casein variant in Korean cattle
A; Reference number: A5068
A; Title: Biochemical characterization of the new beta-casein variant in Korean cattle
A; Reference number: A5068
A; Status: protein sequence not shown
A; Residues: 1-209 < HANI>
A; Status: protein sequence not shown
A; Note: submitted to the Protein Sequence Database, September 1999
A; Note: includes casein phosphopeptide H
A; Status: protein sequence not shown
A; Mescule type: protein
A; Note: lncludes casein phosphopeptide H
A; Status: protein sequence not shown
A; Residues: 1-28 < HANI>
A; Experimental source: strain Korean cattle
C; Stuperfamily: beta-casein
C; Stuperfamily: beta-casein
C; Keywords: milk; phosphoprotein
F; 15, 17, 18, 19, Binding site: phosphate (Ser) (covalent) #status predicted
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R;Petrilli, P.; Pucci, P.; Morris, H.R.; Addeo, F.
Biochem. Biophys. Res. Commun. 140, 28-37, 1986
A;Title: Assignment of phosphorylation sites in buffalo beta-casein by fast atom bomb A;Reference number: A26334; MUID:87048757; PMID:3778448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Bubalus arnee (water buffaio)
C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Sep-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Capra aegggrus hircus (domestic goat)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 23-Feb-1997
C;Accession: JC1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.4%; Score 96; DB 2; Length 209; 83.3%; Pred. No. 3.9e-08; 1ve 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 91; July Pred. No. 4.8e-08; Pred. No. 4.8e-08;
                                                                                              Pred. No. 6.4e-09;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.7%; Score 91; DB 2;
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                                                                                                                                                                                                                                                                                       16 RELEELNVPGEIVESLSSSEESITR 40
                                                                                                                                                                                                                             1 RELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta-casein - water buffalo (fragment)
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                                                                                    84.08;
                                                                                                                                              Conservative
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A: Residues: 1-48 <PET>
C: Superfamily: beta-casein
                                                                               Best Local Similarity
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Best Local Similarity
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                          A; Title: Neoglycoproteins: in vitro introduction of glycosyl units at glutaminesin beta-
A; Reference number: A90489; MUID:85000478; PMID:6148101
A; Reference number: A90489; MUID:85000478; PMID:6148101
A; Residues: 16-224 «YAN»
A; Residues: 16-224 «YAN»
B; Ribadeau-Dumas, B.; Brignon, G.; Grosclaude, F.; Mercier, J.C.
A; Ribadeau-Dumas, B.; Brignon, G.; Grosclaude, F.; Mercier, J.C.
A; Ritle: Structure primmaire de la cassine beta bovine.
A; Reference number: A91191; MUID:72233212; PMID:4557764
A; Rolecule type: protein
A; Residues: 16-131, Q', 133-151, PL', 154-189, E', 191-209, Q', 211-224 «RIB»
A; Residues: 16-131, Q', 133-151, PL', 154-189, E', 191-209, Q', 221-224 «RIB»
A; Roccasidues: 16-131, Q', 133-151, PL', 154-189, E', 191-209, Q', 221-224 «RIB»
A; Roccastlues: 16-131, Q', 133-151, PL', 154-189, E', 191-209, Q', 221-224 «RIB»
A; Roccastlues: 16-131, Q', 133-151, PL', 154-189, E', 191-209, Q', 221-224 «RIB»
A; Note: article in French with an English abstract
A; Reference number: A91192; MUID:7224259; PMID:5064450
A; Note: article in French with an English abstract
A; Note: article in French with an English abstract
A; Note: article in French with an English abstract
A; Note: article in French with an English abstract
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A; Residues: 16-81,'H',83-131,'Q',133-151,'PL',154-189,'E',191-209,'Q',211-224 <VA1>
A; Residues: 16-81,'H',83-131,'Q',133-151,'PL',154-189,'E',191-209,'Q',211-224 <VA1>
A; Accession: C91192
A; Molecule type: protein
A; Residues: 16-81,'H',83-131,'Q',133-151,'PL',154-189,'E',191-209,'Q',211-224
A; Molecule type: protein
A; Residues: 16-51,'M',53-81,'H',83-131,'Q',133-151,'PL',154-189,'E',191-209,'Q',211-224
A; Molecule type: protein
A; Residues: 16-51,'M',53-81,'H',83-131,'Q',133-151,'PL',154-189,'E',191-209,'Q',211-224
A; Residues: 16-51,'M',53-81,'H',83-131,'Q',133-151,'PL',154-189,'E',191-209,'Q',211-224
A; Residues: 16-51,'M',53-81,'H',83-131,'Q',33-151,'PL',154-189,'E',191-209,'Q',211-224
A; Residues: 16-51,'M',53-81,'H',83-131,'Q',33-151,'PL',154-189,'E',191-209,'Q',211-224
A; Residues: 16-51,'M',53-81,'H',83-131,'Q',133-151,'PL',154-189,'E',191-209,'Q',211-224
A; Residues: 16-51,'M',53-81,'H',83-131,'Q',133-151,'PL',154-189,'E',191-209,'Q',211-224
A; Residues: 16-51,'M',53-81,'H',83-131,'Q',133-151,'PL',154-189,'E',191-209,'Q',211-224
A; Reference number: A90739; MOTD: 71-225217; PRD: 4997616
A; Note: article in French with an English abstract
A; Molecule type: protein
A; Molecule type: p
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F.16-224/Product: sequence *status experimental <MAT>
F.16-32,33,34/Aniding site: phosphate (Ser) (covalent) (by casein kinase II) *status experimental characters of the status experimental characters of the sphate (Ser) (covalent) (by casein kinase II) *status experimental characters of the status of the sta
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A;Residues: 118-120, Q',122-124 <VA3>
A;Residues: 118-120, Q',122-124 <VA3>
B;Experimental source: A3 variant
B;Simons, G; van den Heuvel, W; Reynen, T.; Frijters, A.; Rutten, G.; Slangen, C.J.;
Protein Eng. 6, 763-770, 1993
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R; Grosclaude, F.; Mahe, M.F.; Voglino, G.F.
A; Experimental sources and variant
R; Grosclaude, F.; Mahe, M.F.; Voglino, G.F.
A; Title: Le variant betae et le code de phosphorylation des caseines bovines.
A; Reference number: A91413; MuID:75005247; PMID:4411121
A; Note: article in French with an English abstract
A; Accession: A9143
A; Molecule type: protein
A; Residues: 48-50, K', 52-63 <VAE>
A; Experimental source: E variant
A; Note: 50-Ser is phosphorylated
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A; Cross-references: GB:S67277; NID:9459291; PIDN:AAB29137.1; PID:9459292
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A:Introns: 17/3; 26/3; 35/3; 43/3; 57/3; 223/3
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Biochemistry 23, 3759-3765, 1984
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C; Keywords: milk; phosphoprotein
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C; Accession: B96502
R; Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon R; Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chi, C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Chi, C.M.; Hughes, B.; Hutzar, L. ansen, N.F.; Hughes, B.; Hutzar, L. A; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, Nature 408, 816-820, 2000
A; Athors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, Raizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallc Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F28H19.8 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
A; Molecule type: nucleic acid
A; Residues: 1-232 <ALE>
A; Experimental source: mammary gland
A; wote: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:110891, NCBIP:110895)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.7%; Score 48; DB 2; Length 640; 50.0%; Pred. No. 9.6;
                                                                                                                                                                                              63.8%; Score 67; DB 2; Length 232; 62.5%; Pred. No. 0.0024; Live 0; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 EELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                         1 RELEELNVPGEIVEXLXXXEESIT 24
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                                                                                                                                                                                                                                                Local Similarity 62.5% nes 15; Conservative
                                                                                                                                                              C; Superfamily: beta-casein
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-640 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: B96502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: all3289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: F28H19.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics
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                                                                                                                                                                                                                                                                                      Matches
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C; Keywords: milk; phosphoprotein
F;1-15/Domain: signal sequence #status experimental <MAT>
F;16-222/Froduct: beta-casein #status experimental <mar/>F;16-222/Froduct: beta-casein #status
F;30,32,33,34,50/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A32979

Beta-caseln precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis anies, Ovis aries, Ovis orientalis aries, Ovis orientalis aries, Ovis orientalis aries, A2979; A2979; A2979; A2979; A2979; A2979; A2979; A2979; MUD:89375530; PMID:2505862
A;Reference number: A32979
A;Accession: A32979
A;Accession: A32979
A;Accession: A32979
                                         R;Roberts, B.; DiTullio, P.; Vitale, J.; Hehir, K.; Gordon, K. 60 and L. 255-262, 1992
Rene 121, 255-262, 1992
A;Title: Cloning of the goat beta-casein-encoding gene and expression in transgenic mice
A;Reference number: JC1384; MUID:93077039; PMID:1446822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Cypecies: Sus scrofa domestica (domestic pig)
Cypecies: Sus scrofa domestica (domestic pig)
Cypecies: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 03-May-1996
Cypecession: A48384
B.Alexander, Lu.; Beattie, C.W.
Anim. Genet. 23, 369-371, 1992
A.Title: The sequence of porcine beta-casein cDNA.
A;Reference number: A48384; MuID:92367961; PMID:1503277
A;Recession: A48384
A;Accession: A48384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-222 CPRO>
A; Residues: 1-222 CPRO>
A; Cross-references: GB:X16482; NID:g1210; PIDN:CRA34502.1; PID:g1211
A; Note: the authors translated the codon CAC for residue 160 as Lys
A; Note: the authors translated, J.C.
Bur J. Biochem. 90, 286-297, 1979
Eur J. Biochem. 99, 286-297, 1979
A; Title: The primary structure of the ovine beta-caseins.
A; Reference number: A29173; MUID:80046695; PMID:499202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.4%; Score 76; DB 2; Length 222 70.8%; Pred. No. 7.7e-05; tive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 76; DB 2; Lengtn 222
Pred. No. 7.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A;Residues: 16-69, 'r',71-77,'p',79-81,'A',83-222 <RIC>
C;Superfamily: beta casein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                        A;Introns: 17/3; 26/3; 35/3; 45/3; 57/3; 221/3
A;Introns: 17/3; beta-casein
C;Keywords: milk; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RELEELNVPGEIVEXLXXXEESIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 REQEELNVVGETVESLSSSEESIT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RELEELNVPGEIVEXLXXXEESIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 REQEELNVVGETVESLSSSEESIT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.4%;
70.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                              A; Cross-references: GB:M90556
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Matches 17; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-222 <ROB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                     A; Accession: JC1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                  A; Gene: CSN2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                             C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
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Gaps

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9; Indels

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R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irinakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Taba DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MulD:21595285; PMID:11759840
A; Status: preliminary
A; Status: preliminary
                         C; Species: Nostoc sp. Arrain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 c; bate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 c; Accession: AB2217
                                                                                                                                                                                                                                                                                                                                                                                                                              A.Residues: 1-1289 <KUR>
A.Residues: 1-1289 <KUR>
A.Cross-references: GB:BA000019; PIDN:BAB74988.1; PID:917132384; GSPDB:GN00179
A.Experimental source: strain PCC 7120
hypothetical protein all3289 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.8%; Score 47; DB 2; Length 1289;
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 28-Jul-2000
C;Accession: B7264
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; T
BNA Ress. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-492 <MTH>
A;Cross-references: GB:AE000937; GB:AE000666; NID:g2622974; PIDN:AAB86316.1; PID:g262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: B72654
A; Stetus: preliminary
A; Molecule type: DNA
A; Residues: 1-438 < KAN>
A; Cross references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79634.1; PID:g5104319
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C. Superfamily: Methanococcus fumarate reductase; ferredoxin [2Fe-2S] homology C. Keywords: 2Fe-2S; metalloprotein; oxidoreductase C. Seywords: 2Fe-2S; metalloprotein; oxidoreductase F:57,62,65,77/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A. Status: preliminary, nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                          probable histidyl-tRNA synthetase APE0662 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bPS2 protein homolog (bps2) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Gene: App0662
C;Superfamily: histidine-tRNA ligase; histidine-tRNA ligase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 56.2%; Score 46; DB 2; Length 438; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.9%; Score 45; DB 1; Length 492; 61.5%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A69000; MUID: 98037514; PMID: 9371463
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3; Mismatches
                                                                 32 KEFEKIHIPNEIVEEILVRLPVKSLTR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 RELERLGLPGSTVERI 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 9: Conserv
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                                                                                           qq
                                                                                                                                                                                                                                                                 JT0564
Deta-casein precursor - rabbit
C; Specias: Oryctolagus cuniculus (domestic rabbit)
C; Specias: Oryctolagus cuniculus (domestic rabbit)
C; Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 13-Aug-1999
C; Accession: JT0564; S02043
R; Thepot. D: Devinoy, E:; Fontaine, M.L.; Houdebine, L.M.
R; Title: Structure of the gene encoding rabbit beta-casein.
A; Reference number: JT0564; MUID:91153663; PMID:1999295
A; Residues: 1-28 crHRs
A; Molecule type: DNA
A; Residues: 1-28 crHRs
A; Cross-references: GB:M33582; NID:9164786; PIDN:AAA31168.1; PID:9164787
A; Cross-references: GB:M33582; NID:9164786; PIDN:AAA31168.1; PID:9164787
A; Cross-references: GB:M3582; NID:9164786; PIDN:AAA31168.1; PID:9164787
A; Title: Sequence of the rabbit beta-casein cDNA: comparison with other casein cDNA A: Accession: CNAA;
A:Accession: CNAA; MUID:89098330; PMID:3211753
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A; Cross-references: GB:AE002093; NID:94406785; PIDN:AAD20095.1; GSPDB:GN00139
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein At2902030 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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A.Molecule type: mRNA
A.Residues: 1-86, 1', 88-228 <SCH>
A.Cross-references: EMBL:X13043; NID:91517; PIDN:CAA31449.1; PID:91518
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                                                                    Indels
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Pred. No. 9.7;
8; Mismatches 7; Indels
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C:Keywords: calcium, milk; phosphoprotein
F:1-15/Domain: signal sequence #status predicted <SIG>F:16-228/Product: beta casein #status predicted <MAI>
                                                          Mismatches
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3; Mismatches
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R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-218 < KAM>
A; Residues: 1-218 < KAM>
A; Residues: 1-218 < KAM>
A; Cross-references: GBAP000001; NID: 93236128; PIDN: BAA29199.1; PID: 93256516
A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBank C; Genetics:
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandon, Q.; Singh, R.K.; Sorzera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Rescription: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: A90394
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C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C; Accession: 132463
C; Accession: T32463
A; Blanchard, M.; Gattung, S.; Sansone, J.
Submitted to the EMBL Data Library, September 1997
Submitted to the EMBL Data Library, September 1997
A; Reference number: 221173
A; Reference number: 221173
A; Accession: T32463
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-807 < ELAA>
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C;Species: Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 28-Jul-2000
C;Accession: H71233
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42.9%; Score 45; DB 2; Length 807;
Best Local Similarity 45.0%; Pred. No. 39;
Matches 9; Conservative 4; Mismatches 7; Indels
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45.5%; Pred. No. 27;
tive 3; Mismatches 9; Indels
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A; Introns: 383/3; 434/2; 507/3; 550/3; 648/3; 759/2
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Matches 10; Conserva
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A; Residues: 1-587 <KUR>
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SECUENCE OF 68-105 FROM N.A.
MEDLINE=85155504; PubMed=6397405;
MEDLINE=81155504; Reishilite D.R., Bayev A.A., Akhundova A.A.,
Sulimova G.E., Judinkova E.S., Gorodetsky S.I.;
"Identification of bacterial clones encoding bovine caseins by direct immunological screening of the cDNA library.";
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"The beta E variant and the phosphorylation code of bovine caseins.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20154951; PubMed=10690361;
Han S.K., Shin Y.C., Byun H.D.;
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Dong C., Ng.Kwai Hang K.F.;

"Characterization of a non-electrophoretic genetic variant of beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 170-184 FROM N.A.
MEDLINE=83182023; PubMed=6897774;
Willis I.M., Stewart A.F., Caputo A., Thompson A.R., McKinlay A.G.;
"Construction and identification by partial nucleotide sequence analysis of botine casein and beta-lactoglobulin cDNA clones.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mapping and mass spectrometric analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Visser S., Slangen C.J., Lagerwerf F.M., Van Dongen W.D.,
Haverkamp J.,
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SEQUENCE OF 16-224 (VARIANT A2)
MEDLINE=72233212; PubMed=4557764;
                                                                                                  VARIANTS A1; B AND C.
MEDLINE=72214259; PubMed=5064450;
                                                                                                                                                                                                                    SEQUENCE OF 118-124 (VARIANT A3).
MEDLINE=71252171; PubMed=4997616;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 48-63 (VARIANT E).
MEDLINE=75005247; Pubmed=4411121;
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MFDLINE=86014005; PubMed=3900695;
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MEDLINE-96118672; Pubmed=7496485;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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Blochemistry 23:3759-3765(1984).
- FOUNTION: IMPORTANT ROLE IN DETERMINATION OF THE SURFACE
PROPERTIES OF THE CASEIN MICELLES.
-1 SUBCELLULAR LOCATION: Extracellular.
-1 TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-1 POLYMORPHISM: LEU-152 IS PRESENT IN THE VARIANTS F AND G; GLN-190
AND GLU-210 ARE PRESENT IN THE VARIANT F SEQUENCE SHOWN IS
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E -> C (IN VARIANT H)
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                                                                                                                                                                                                              WWW="http://www.expasy.org/spotlight/articles/spt1t016.html".
                                                                                                                                                                                                                                                                                                                                                                              Yan S.B., Wold F.; "Neoglycoproteins: in vitro introduction of glycosyl units at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGPFPIIV -> DPSLLL (IN REF. 1). FOBBDD8148A238AE CRC64;
                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE BETA-CASEIN FAMILY.
-!- DATABASE: NAME-Protein Spotlight;
NOTE-ISSUE 16 of November 2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPSLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVRGPFPIIV ->
                                                                                                                                                                                                                                                                                                                                                    EMBL, M16645, AAA30480.1;
EMBL, M15132, AAA30430.1;
EMBL, K01087, AAA30481.1;
EMBL, X06559; CAA29658.1;
EMBL, S77277, AAB29137.1;
EMBL, AF104929; AAD09813.1;
EMBL, AF104928; AAD09813.1;
EMBL, AF104928; AAD09813.1;
EMBL, AF104928; AAB59254.1;
MEDLINE=85000478; PubMed=6148101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25107 MW;
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Length 224;

Score 101; DB 1; Pred. No. 3.7e-09;

96.2%; 84.0%;

Best Local Similarity

Query Match

CARBOHYDRATE-LINKAGE SITES.

16 RELEELNVPGEIVESLSSSEESIT 39

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STANDARD;
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nes 17; Conserva
                                                                                     Beta casein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CASB_SHEEP
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MOD_RES
MOD_RES
                                       CASB_CAPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
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                              CASB_CAPHI
                      RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BETA CASELA.

PHOSPHORYLATION (BY SIMILARITY).

O-LINKED (GALNAC...) (BY SIMILARITY).

O-LINKED (GALNAC...) (BY SIMILARITY).

O-LINKED (GALNAC...) (BY SIMILARITY).

O-LINKED (GALNAC...) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Gaps
                                                                                                                                                                                                                                                                                    Bubalus bubalis (Domestic water buffalo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14FD3687DD17C5A9 CRC64;
                                                                                                                                                                                                                            TISSUB-Mammary gland;
Klotz A., Krause I., Einspanier R.;
"Isolation of mRNA from buffalo milk.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O-LINKED (GALNAC. ..)
O-LINKED (GALNAC. ..)
O-LINKED (GALNAC. ..)
O-LINKED (GALNAC. ..)
M -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE: PS00363; caseins; 1.
PROSITE: PS00306; CASEIN ALPHA_BETA: 1.
Milk: Phosphorylation; Glycoprotein; Signal.
1.15
BY SINGLARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                          224 AA
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RELEELNVPGEIVEXLXXXEESIT 24
                                                                                           PRT;
                     1 RELEELNVPGEIVEXLXXXEESITR 25
                                 EMBL; AJ005165; CAA06408.1; -. EMBL; AJ005432; CAA06535.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25106 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001588; Casein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                         Bovidae; Bovinae; Bubalus.
NCBI_TaxID=89462;
     21; Conservative
                                                                                            STANDARD;
                                                                                                                                              Beta casein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95
183
117
224 AA;
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                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ005432;
                                                                                            CASB_BUBBU 5
Q9TSI0; 062824;
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        Matches
                                                                           RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidea; Caprinee; Caprinee; Caprinee; Capra.
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-Saanen; TISSUE-Blood;
STRAIN-S3077039; PubMed=1446822;
MEDLINE=93077039; PubMed=1446822;
Roberts B., Ditullio P., Vitale J., Hehir K., Gordon K.;
"Cloning of the goat beta-casein-encoding gene and expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96AE17746A01CD05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00363; caseins; 1.
PE; PS00306; CASEIN_ALPHA_BETA; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.4%; Score 76; DB 1; 70.8%; Pred. No. 4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1989 (Rel. 12, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pred. No. 4e-0
0; Mismatches
                                         01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
222 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BETA CASEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RELEELNVPGEIVEXLXXXEESIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 REQEELNVVGETVESLSSSEESIT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M90561; AAA30906.1; ...
EMBL; M90556; AAA30906.1; JOINED.
EMBL; M90557; AAA30906.1; JOINED.
EMBL; M90560; AAA30906.1; JOINED.
EMBL; M90560; AAA30906.1; JOINED.
     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR, JC1384, JC1384.
InterPro, IPR001588; Casein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                  Ovis aries (Sheep).
Wakaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                           N 15.0

N 16.0

N 16.0

N 16.0

N 16.0

N MEDLINE-80046695; PubMed-499202;

N MEDLINE-80046695; PubMed-499202;

N Hichardson B.C., Mercier J.-C.;

Eur. J. Blochem. 99:288-297(1979),

- FUNCTION: IMPORTANT ROLE IN DETERMINATION OF THE SURFACE

CC -- SUBCELLULAR LOCATION: Extracellular.

CC -- SIMILARITY: BELONGS TO THE BETA-CASEIN FAMILY.
                                                                                                                                                                                                         MEDLINE=93197013; PubMed=7890174; Provot C., Persuy M.A., Mercier J.-C.; Complete sequence of the ovine beta-casein-encoding gene and interspecies comparison."; Gene 154:259-263(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                   Provot C., Persuy M.A., Mercier J.-C., "Complete nucleotide sequence of ovine beta-casein cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 76; DB 1; Length 222;
Pred. No. 4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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PHOSPHORYLATION (POTENTIAL)
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061B4424DCB49EB1 CRC64;
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  (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A291,5, A32979.

PIR; A32979; A32979.

PIR; PS07363; Casein.

Pfam; PF00363; Caseins; 1.

PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.

PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
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PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BETA CASEIN.
                                                                                                                       MEDLINE=89375530; PubMed=2505862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RELEELNVPGEIVEXLXXXEESIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 REQEELNVVGETVESLSSSEESIT 39
                                                                                                                                                                        Biochimie 71:827-832(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X16482; CAA34502.1; -. EMBL; X79703; CAA56139.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24875 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.8%;
                                                                                                                                                           inter-species comparison
              Beta casein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222
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32
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70
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 AA;
 01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
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P39037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
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                                                                                                                                                        Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) (POTENTIAL).
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0
                                                                                                                                                                                                                                                                                                                              Alexander 1.3. Beattie C.W.;

"The sequence of portine beta-casein cDNA.";

Anim. Genet. 23:369-371(1992).

"PROPERTIES OF THE CASEIN MICELLES.

"SUBCELLUIAR LOCATION: Extracellular.

"TISSUE SPECIFICITY: MAMMARY GLAND; MILK.

"SIMILARITY: BELONGS TO THE BETA-CASEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETA CASEIN.
HOSPHORYLATION (BY SIMILARITY)
PHOSPHORYLATION (BY SIMILARITY)
PHOSPHORYLATION (BY SIMILARITY)
PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 67; DB 1; Length 232;
Pred. No. 0.0012;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SOMALI; TISSUE-Mammary gland;
MEDLINE-98291310; PubMed=9627840;
Kappeler S., Farah Z., Puhan Z.;
"Sequence analysis of Camelus dromedarius milk caseins.";
J. Dairy Res. 65:209-222(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (PC
6284850F40F7365C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | PROSITE; | PROMOSON, | PROSITE; | PROSIDE, | PROSIDE,
     (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                          TISSUE=Mammary gland;
MEDLINE=92367961; PubMed=1503277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 KAKEELNASGETVESLSSSEESIT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001588; Casein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X54974; CAA38718.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.8%;
62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                             Beta casein precursor.
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                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                  Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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01-FEB-1995
01-FEB-1995
01-NOV-1997
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CASB_CAMDR
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                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "sequence of the rabbit beta-casein cDNA: comparison with other
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--- SUBCELLULAR LOCATION: EXLETGCELLULAR.
--- TISSUE SPECIFICITY: MAMMARY GLAND: MILK.
--- SIMILARITY: BELONGS TO THE BETA-CASEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
A0F9F41D2EA7C518 CRC64;
-i- FUNCTION: IMPORTANT ROLE IN DETERMINATION OF THE SURFACE PROPERTIES OF THE CASEIN MICELLES (BY SIMILARITY).
-i- SUBCELLIOLAR LOCATION: EXETACEDILLAR.
-i- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-i- SIMILARITY: BELONGS TO THE BETA-CASEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.2%; Score 58; DB 1; Length 232; 50.0%; Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thepot D., Devinoy E., Fontaine M.L., Houdebine L.M., "Structure of the gene encoding rabbit beta-casein."; Gene 97:301-306(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRLIN-New Zealand white; TISSUE-Mammary gland; MEDLINE-89098330; PubMed=3211753;
                                                                                                                                                                                                                                        EMBL; AJ012630; CAA10079.1; -.
InterPro; IPR001588; Casein.
Pfam; PF00363; Caseins; 1.
PROSITE; PS00306; CASEIN_ALPHA_BETA; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 10, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                Phosphorylation; Glycoprotein; Signal.
L 1 15 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    casein cDNA sequences.";
Nucleic Acids Res. 16:111814-11814(1988).
                                                                                                                                                                                                                                                                                                                                               BETA CASEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Liver;
MEDLINE=91153663; PubMed=1999295;
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33 33 PHC
34 34 PHC
232 AA; 26218 MW; A
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SEQUENCE
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-!- SUBGELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-11 AMINOACYL-TRNA SYNTHEFASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE=99310339; Pubbmed=10382966; Yamazaki S., Haikawa Y., Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Kawarabayasi Y., Hino Y., Horikawa H., Baba S.-I., Ankai A., Kosugi H., Jin-no K., Takahashi M., Sekine M., Inshijima K., Nakazawa H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takaniya M., Masuda S., Funahashi T., Tanaka T., Kubota K., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
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                                                                                                                                                                                                                                                                                                                                                                                     Length 228;
                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                             228 BETA CASEIN.
30 PHOSPHORYLATION (POTENTIAL).
32 PHOSPHORYLATION (POTENTIAL).
33 PHOSPHORYLATION (POTENTIAL).
34 PHOSPHORYLATION (POTENTIAL).
87 I -> T (IN REF. 2).
87 I -> T (IN REF. 2).
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Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococcaceae; Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                               TE; PS00306; CASEIN_ALPHA_BETA; 1.
Phosphorylation; Glycoprotein; Signal.
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                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                43.8%; Score 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            crenarchaeon, Aeropyrum pernix Kl.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP000060; BAA79634.1; -. HSSP; 032422; 1QE0.
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30-MAY-2000 (Rel. 39, Last sequ
16-0CT-2001 (Rel. 40, Last anno
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16 REKEQLSVPTEAVGSVSSSEE 36
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                                                                                                                                                  PIR, JT0564, JT0564.
Interpro, IPR001588; Casein.
Pfam; PF00363; Caseins; 1.
                                                                                                               EMBL; X13043; CAA31449.1; -. EMBL; M33582; AAA31168.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   47.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
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                                                                                                                                                                                                                                                                                                                                                               228 AA;
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CONFLICT
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MOD_RES
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InterPro; IPR002106; AALRNA_ligaseII.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR004156; Hiss.
InterPro; IPR00314; TRNA-synt_2b.
Pfam; PF00587; tRNA-synt_2b; 1.
Pfam; PF03129; HGTP_anticodon; 1.
PTGRRAMs; TIGRR0442; hiss; 1.
PR05ITE; PS50862; AA_TRNA_LIGASE_II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                            TRII_ECOLI STANDARD; PRT; 1756 AA.
P14565; Q51811;
01-JAN-11990 (Rel. 13, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TraI protein (DNA helicase I) (EC 3.6.1.-) [Contains: Trai* protein].
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Frost L.S., Ippen-Ihler K., Skurray R.A.;
"Analysis of the sequence and gene products of the transfer region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jalajakumari M.B., Manning P.A.;
"Nucleotide sequence of the traD region in the Escherichia coli F sex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimizu H., Saitch Y., Suda Y., Uehara K., Sampei G., Mizobuchi K.; "Complete nucleotide sequence of the F plasmid: its implications for organization and diversification of plasmid genomes."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90317835; PubMed-2164585;
Yoshioka Y., Fujita Y., Ohtsubo E.;
"Nucleotide sequence of the promoter-distal region of the tra operon of plasmid R100, including traI (DNA helicase I) and traD genes.";
[6] Wol. Biol. 214:39-53(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gordon M.P., "Nucleotide sequence of the tral (helicase I) gene from the sex
                                                                                                                                                                                     43.8%; Score 46; DB 1; Length 438; 56.2%; Pred. No. 5.9;
                                                                                                                                                                                                                         5; Indels
                                                                                                                                                     438 AA; 49111 MW; ECCE67F59A9FB7BC CRC64;
                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol. 172:4127-4131(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90299847; PubMed-2163400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94359430; PubMed=7915817;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-150 FROM N.A.
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                                                                                                                                                                                                                   Conservative
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Best Local Similarity
                                                                                                                                       Complete proteome
SEQUENCE 438 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex factor.
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                             Penfold S.S., Simon J., Frost L.S.;

Regulation of the expression of the tram gene of the F sex factor of Escherichia coli.";

Mol. Microbiol. 20:549-58(1996).

-- FUNCTION: TRAI HAS BEEN IDENTIFIED AS DNA HELICASE I AND IT ALSO HAS AN ADDITIFIONAL ACTIVITY OF SITE-SPECIFIC NICKING AT ORIT. DNA HELICASE I IS A POTENT DNA-DEPENDENT ATPASE.

-- ALTERNATIVE PRODUCTS: THE TRAI* PROTEIN ARISES FROM AN INTERNAL IN-FRAME TRANSLATIONAL START IN TRAI.

-- SIMILARITY: STRONG TO TRAI OF PLASMID INCFII R100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EcoGene; EC40119; tral
Plasmid; Helicase; ATP-binding; DNA-binding; Conjugation; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Rat prostatic binding protein: the complete sequence of the C2 gene and its flanking regions.";
Nucleic Acids Res. 15:1627-1641(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
07-JONAY-2000 (Rel. 39, Last annotation update)
Prostatic steroid-binding protein C2 chain precursor (Prostatein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87146484; PubMed=2881277;
Delaey B., Dirckx L., Decourt J.-L., Claessens F., Peeters B.,
Rombauts W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 1; Length 1756;
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 MQDGSN -> CRMAVT (IN REF. 4).
192015 MW; AA07D61DB2BFD9FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOR TRAI*.
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternative initiation; Complete proteome.
CHAIN 1 1756 TRAI* PROTEIN.
CHAIN 955 1756 TRAI* PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=83209619; PubMed=6343081;
Peeters B., Heyns W., Mous J., Rombauts W.;
                                                                                                                                                                                                                                                                                                                                                                 EMBL; M54796; AAA98086.1; --
EMBL; U01159; AAC44186.1; --
EMBL; AP001918; BAA97974.1; --
EMBL; M29254; AAA83930.1; ALT_INIT.
EMBL; X57430; CAA40677.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
SEQUENCE OF 955-1756 FROM N.A. MEDLINE=96347127; Pubmed=8736534;
                                                                                                                                                                                                                                                                                                                                                    EMBL; M54796; AAA98085.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   U01159; AAC44187.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                961 VPGELMEKLTSGORAATR 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 VPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 44.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1756 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; PS0068; BVECAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2] SEQUENCE OF 21-112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INIT_MET
NP_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSC2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
PSC2_RAT
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                                                                                                                                                                                      GLYCOPROTEIN OF VENTRAL PROSTATE GLAND.
SUBGNIT: PROSTATEIN IS COMPOSED OF THREE DIFFERENT PEPTIDES CALLED
C1, C2 AND C3. THESE FORM COVALENT C1:C3 (F) AND C2:C3 (S)
HETERODIMERS WHOSE NONCOVALENT ASSOCIATION FORMS TETRAMERIC
(C1:C3/C3:C2) PROSTATEIN MOLECULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha-1,4 glucan phosphorylase, L-2 isozyme, chloroplast precursor (EC 2.41.1.) (Starch phosphorylase L-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSTATIC STEROID-BINDING PROTEIN C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERCHAIN (WITH C3) (PROBABLE).
INTERCHAIN (WITH C3) (PROBABLE).
INTERCHAIN (WITH C3) (PROBABLE).
MISSING (IN REF. 3).
I -> T (IN REF. 3).
VHLQINFPRGRWFSEIN -> YGYK (IN REF.
"Structural studies on rat prostatic binding protein. The primary structure of component C2 from subunit S.";
Eur. J. Biochem. 132:669-679(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                         Parker M., Needham M., White R.; Parker M. Needham M., Whotein: gene duplication and steroid "prostatic steroid binding protein: gene duplication and steroid
                                                                                                                                                                                                                                                                            -:- SUBCEDIULAR LOCATION: Secreted.
-:- PTM: LINKED BY THREE DISULFIDE BONDS TO C3.
-- PTM: LINKED BY THREE DISULFIDE BOND TO C3.
-- PTM: LINKED BY THREE DISULFIDE BOND TO C3.
-- PTM: LINKED BY THREE DISULFIDE BOND TO C3.
-- MILLE DISULFIDE BOLD THREE DISULFIDES.
-- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN
                                                                                                                                                                        FUNCTION: PART OF PROSTATEIN WHICH IS THE MAJOR SECRETORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 1; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DA65A6A82E677864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00403; UTEROGLOBIN_1; FALSE_NEG.
PROSITE; PS00404; UTEROGLOBIN_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOCKED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000329; Uteroglobin.
                                                                                SEQUENCE OF 1-100 FROM N.A.
MEDLINE=82220075; PubMed=6896362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12828 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V01256; CAA24569.1; -. J00776; AAA51641.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X05034; CAA28708.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steroid-binding; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RELEELNVPGEIVE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 RELEEFDAPPEAVE 61
                                                                                                                                                     binding.";
Nature 298:92-94(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A26671; A26671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A03251; BORT2
                                                                                              MEDLINE=82220075;
                                                                                                                                                                                                                                                                                                                                                                             SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHS2_SOLTU
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-89243175; PubMed-2524126;
Kinney R.M., Johnson B.J.B., Welch J.B., Tsuchiya K.R., Trent D.W.;
"The full-length nucleotide sequences of the virulent Trinidad donkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nonstructural polyprotein [Contains: Nonstructural protein NSP1;
Nonstructural protein NSP2; Nonstructural protein NSP3; Nonstructural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPR000811; GT_35.

Pfam; pF00343; phosphorylase; 1.

PROSTIE; PS00102; PHOSPHORYLASE; 1.

Transferase; Glycosyltransferase; Carbohydrate metabolism;

Allosteric enzyme; Pyridoxal phosphate; Transit peptide; Chloroplast;
                                                                                      STRAIN-CV. Desiree; TISSUE-Leaf;
MEDLINE-95201249; PubMed-7894019;
Sonnewald U. Basner A., Greve B., Steup M.;
Sooncewald U. Basner A., Greve B., Steup M.;
A second L-type isozyme of potato glucan phosphorylase: cloning,
antisense inhibition and expression analysis.";
Plant Mol. Biol. 27:56'-576(1995).
-: FUNCTION: PHOSPHOYLASE IS AN IMPORTANT ALLOSTERIC ENZYME IN
CARBOHYDRATE METABOLISM. ENZYMES FROM DIFFERENT SOURCES DIFFER IN
THEIR REGULATORY MECHANISMS AND IN THEIR NATURAL SUBSTRATES.
HOWEVER, ALL KNOWN PHOSPHORYLASES SHARE CATALYTIC AND STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venezuelan equine encephalitis virus (strain Trinidad donkey).
Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
                                                                                                                                                                                                                                                                                            --- CATALYTIC ACTIVITY: {(1,4)-alpha-D-glucosyl}(N) + phosphate = {(1,4)-alpha-D-glucosyl}(N-1) + alpha-D-glucose 1-phosphate. --- COFACTOR: PYRIDOXAL PHOSPHATE. --- SUBCELLULAR LOCATION: Chloroplast; amyloplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALPHA-1,4 GLUCAN PHOSPHORYLASE, L-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                      -i - SIMILARITY: BELONGS TO THE GLYCOGEN PHOSPHORYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 1; Length 974;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               820 820 PYRIDOXAL PHOSPHATE (BY SAT
974 AA; 110700 MW; 5EF8A23C237463D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHLOROPLAST (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 2492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 44;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 RILDNVEIPSSVLELLIKAEES 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RELEELNVPGEIVEXLXXXEES 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amyloplast; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X73684; CAA52036.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.0%;
                                                                                                                                                                                                                                                                                                                                                                               -i- TISSUE SPECIFICITY: LEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 36.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=11038;
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                               NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLN_EEVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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 STRAIN-168 / JH642;
STRAIN-168 / JH642;
STRAIN-57124195; PubMed-8959508;
MiZuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
0
                                                                                                                                                                                                                                                                                                                               Polyprotein; Nonstructural protein; RNA-binding; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-168 / JH642;
MEDLINE-95219086; PubMed=7704261;
Takemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;
"Complete nucleotide sequence of a skin element excised by DNA rearrangement during sporulation in Bacillus subtilis.";
Microbiology 141:323-327(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 1; Length 2492;
Pred. No. 1.2e+02;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                          NONSTRUCTURAL PROTEIN NSPI.
NONSTRUCTURAL PROTEIN NSP2.
NONSTRUCTURAL PROTEIN NSP3.
NONSTRUCTURAL PROTEIN NSP4.
                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL).
W: 1BAD415B70DC3FA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|:|||::|: | |: |
|1174 EKLSVPGKMVDWLSDRPEATFR 1195
                                                                                                                                                                                                                                                                                             PF01661; Alpp; 1.
PF01707; Peptidase_C9; 1.
; SM00506; Alpp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                2492 AA; 277902 MW;
                                                                                                                                                                                      EMBL; J04332; AAB02518.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                           41.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 EELNVPGEIVEXLXXXEESITR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein yqcB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    1329
1879
2492
                                                                                                                                                                                                     PIR; A31467; MNWVTD.
MEROPS; C09.001; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1423;
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ID YQCB_BACSU
                                                                                                                                                                                                                                                                                                                                             Helicase.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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qq
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RA MUNITE-WORDAGE-938437;

RA AZEVEDO W., BETTERO M.G., BESIERS P., BOLOTIN A., Alloni G.,

RA ERENTISS R., DOUSTBET L., BRADS A., Braun M., Brignell S.C., Bron S.,

RA DEDUILLE-WILL B. BRADS A., Braun M., Brignell S.C., Bron S.,

RA Choi S.K., Coddani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA DEDIZOT F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Glims Y.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Glims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Gliseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

Medina N., Mellado R.P., Mixuno M., Moestl D., Nakai S., Noback M.,

RA Persecan E., Pujic P., Purnelle B., Porwollik S., Prescott A.M.,

RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Raynolds S.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Tageuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takenaru K.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

RA Winters P., Wabmutt R., Wadler E., Wedler H., Waltzenegger T.,

RA Winters P., Wabmutt R., Vashikawa H., Danchin A.,

RA Toshida K., Yoshikawa H.F., Zunstein E., Yoshikawa H., Danchin A.,

RA Toshila S.,

RY P., The Complete C. The Gram-Positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medigue C., Moszer I., Viari A., Danchin A.;
"Analysis of a Bacillus subtilis genome fragment using a co-operative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
  the Bacillus subtilis genome containing the skin element and many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6442F65913BB40FE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome
                                           Microbiology 142:3103-3111(1996).
                                                                                                                    MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96084975; PubMed=7489895;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           computer system prototype.";
Gene 165:GC37-GC51(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Complet SEQUENCE 90 AA; 10357 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D32216; BAA06954.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 299117; CAB14537.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                        sporulation genes.
                                                                            SEQUENCE FROM N.A.
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ID UL31 F
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264 AA.

PRT;

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fight H., de Rossi E., Salazar L., Cantoni R., Labo M., Riccardi G., Takilf H.E., Eiglmeier K., Bergh S., Cole S.T.; "Gene arrangement and organization in a approximately 76 kb fragment encompassing the oric region of the chromosome of Mycobacterium
                                                                                                                                                                                                                                                                                                              DEQUENCE OF 85-264 FROM N.A. MEDIANGELINE=91333007; PubMed=1651403; MEDLINE=91333007; PubMed=1651403; MEDLINE=91333007; PubMed=1651403; M.D.; Teo I.A., Griffin B.E., Jones M.D.; Teo I.A., Griffin B.E., Jones M.D.; J. Virol. 65:4670-4680(1991).

-I. SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL31, EHV-1 29, EBV BFLF2, HCMY UL33, AND VZV 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Mycobacterium
                                                                                                                                                                                                  Gompels G.A., Nicholas J., Lawrence G., Jones M., Thomson B.J., Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.; "The DNA sequence of human herpesvirus-6: structure, coding content,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 1; Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pfam: PF02718; Herpes_UL31; 1.
SEQUENCE 264 AA; 30845 MW; 5A0D8D66F0lAAF94 CRC64;
                                                                                   Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chromosomal replication initiator protein dnaA.
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     01-DEC-1992 (Rel. 24, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 15;
6; Mismatches
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InterPro; IPR003868; Herpes_UL31-11ke.
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                                                                                                                                                                                             MEDLINE-95266321; PubMed=7747482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                           Betaherpesvirinae; Roseolovirus.
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                                                                                                                                                                                                                                                                    and genome evolution."; Virology 209:29-51(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=10370;
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P46388;
                                                                                 U37 OR XIRF2
                                                                 Protein U37
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P28865;
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                                                                                                                                                                        Gaps
                                      Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Whogall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.
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DNA replication; DNA-binding; ATP-binding; Complete proteome.
The replication; DNA-binding; ATP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL).
A -> R (IN REF. 1).
, 2D45721D99DEDEAE CRC64;
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35.0%; Pred. No. 30;
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EMBL; AL583917; CAC29509.1; ALT_INIT.
                                  MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR003593; AAA_ATPase.
Interpro; IPR001957; Bac_DnaA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00382; AAA; 1.
TIGREAMS; TIGR00362; DnaA; 1.
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[2]
SEQUENCE FROM N.A.
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CONFLICT
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                           February 11, 2003, 18:13:41; Search time 28.0928 Seconds (without alignments) 183.363 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                        671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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sp_unclassified:*
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sp_invertebrate:*
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sp_rodent:*
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	% Query Match	7.2.7.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.
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Q8vsb0 shigella fl Q9lep9 brassica na Q91af7 escherichia Q9af10 shigella fl Q8xc3 pyrobaculum Q8xry7 ralstonia s Q8xry7 ralstonia s Q8xry7 ralstonia s Q9xi7 aeropyrum p Q9ya77 aeropyrum p Q9ya71 venezuelan Q6594 venezuelan Q6594 venezuelan Q6594 venezuelan Q6594 venezuelan Q6594 venezuelan Q6594 venezuelan Q6594 venezuelan Q6594 venezuelan Q6594 venezuelan	Ogyag3 thermoplasm Qgyuf6 encephalito Qgyuf6 encephalito Qgyuf27 human herpe Qgq36 salmonella Qg273 salmonella Qg5x03 naegleria f Qgbkm2 naegleria f
Q8VSB0 Q9LEP9 Q9LEP9 Q9AEL0 Q8XEV7 Q8XEV7 O58G6 Q8XXIO Q9XA77 Q9WJJ1 Q9WJJ3 Q66594 Q66594	02554/ 02554/ 087463 088V16 097462 095403 082036 082036 095503 099503 099771 099771 099771
100 110 110 110 110 110 110 110 110 110	16 112 112 116 116 5 5 5 11 111
1156 1238 1623 1623 367 369 472 859 983 1879 2481 2493	140 185 259 259 265 293 294 307 506 525 6155
441.0	4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
4444444444444 4444666666666666	4 0 .444444444444444 0UUUUUUUUUUUUUU
117 20 20 22 22 22 26 26 26 30	

## ALIGNMENTS

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Gaps
                                                                                                           Capra hircus (Goat).

Capra hircus (Coat).

Bukaryota: Metazooa; Chordata; Craniata; Vertebrata; Bovoidea;

Mammalla; Eutheria; Cetartiodactyla; Ruminantla; Pecora; Bovoidea;

Bovidee; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                      Length 223;
                                                                                                                                                                                                                                                                                                                                       72.4%; Score 76; DB 6; Length 223
70.8%; Pred. No. 0.00016;
tive 0; Mismatches 7; Indels
                                                                                                                                                                                                        Mang Q., Huang Z., Chen M.J., Huang S.Z., Zeng Y.T.; Submitted (AuG-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF409096; AAK97639.1; -Interpro; IPR001588; Casein. PF00363; caseins? 1.
                                                                                                                                                                                                                                                                                                              35A8BE17746A01DB CRC64;
                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                       BETA-CASEIN.
                                                                                                                                                                                                                                                                                            POTENTIAL.
                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                               1 RELEELNVPGEIVEXLXXXEESIT 24
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CHAIN 16 223 B
SEQUENCE 223 AA; 24992 MW;
                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 70.89
Matches 17; Conservative
                       PRELIMINARY;
                                                                                      Beta-casein precursor.
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                  NCBI_TaxID=9925;
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SIGNAL
                      Q95L76
Q95L76;
RESULT 1
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250 AA.

PRT;

PRELIMINARY;

Q9N2G8

RESULT 2

Q9N2G8

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Watanabe M., Sugano S., Togashi T., Imai J., Uchida K., Yamaguchi R.,
Tateyama S.;
                                                                                                                                                                                       "Molecular cloning and phylogenetic analysis of canine beta-casein."; DNA Seq. 11:295-300(2000).
EMBL; AB035080: BAA55931.1; -
InterPro; IPR001588; Casein.; I
Pfam; PF00363; caseins; 1.
PROSITE; PS00306; CASEIN ALPHA BETA; 1.
PROSITE: 250 AA; 28401 MW; 1D58391E7BE97ED8 CRC64;
                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                                                                         Score 62; DB 6; Length 250;
                                                                                                                                                                                                                                                                                                                     49.5%; Score 52; DB 6; Length 233; 60.0%; Pred. No. 1.5; tive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lenasi T., Rogelj I., Debeljak M., Dovc P.;
"Primary structure of equine beta-casein (b-CN) cDNA.";
Submitted (JUN-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; AF214526; AAG43954.1;
Interpro; IPR001588; Casein.
Pfam; PF00363; caseins; 1.
PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last Sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL. 492A07BD010FBF88 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=HANNOVERIAN; TISSUE=LACTAING MAMMARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 AA.
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1; Mismatches
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233 AA; 26126 MW;
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les 14; Conservative
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                                                                  Canis familiaris (Dog)
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                                                                                                                                     SEQUENCE FROM N.A.
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 Q9N2G8;
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                       Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehher E., Chao O., Chin C., Chiou J., Choi E., Gonzalez A., Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M., Lenz C., Liu A., Liu S., Wukharsky N., Pham P., Sakano H., Shinn P., Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AC006423; AAR63114.1; -
InterPro; IPR001584; Rve.
SEQUENCE 640 AA; 73395 MW; 885DE941A980CD55 CRC64;
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STRAIN-NCIB 9867; TRANSPOSON=TN5563;
MEDLINE-98126538; Pubmed-9465399);
KWONG S.M., YOO C.C., Chubh D., Poh C.L.;
Sequence analysis of plasmid pRA2 from Pseudomonas alcaligenes NCIB 9867 (P25X) reveals a novel replication region.";
FEMS Microbiol. Lett. 158:159-165(1998).
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"Characterization of the endogenous plasmid from Pseudomonas alcaligenes NCIB 9867: DNA sequence and mechanism of transfer.";
J. Bacteriol. 182.81-90(2000).
EMBL: U88088; AAD40349.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeo C.C., Tham J.M., Kwong S.M., Yiin S., Poh C.L.;
"In5563, a transposon encoding putative mercuric ion transport
proteins located on plasmid pRA2 of Pseudomonas alcaligenes.";
FEMS Microbiol. Lett. 165:253-260(1998).
                                                                                                                                                                                                                                                                                                                                          45.7%; Score 48; DB 10; Length 640; 50.0%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                9; Indels
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SEQUENCE 291 AA; 32661 MW; 970E473ADC8F479D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 32.7 kDa protein.
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Pred. No. 13;
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SEQUENCE FROM N.A.
STRAIN-NCIB 9867; TRANSPOSON=TN5563;
MEDLINE-98415121; Pubmed-9742696,
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STRAIN-NCIB 9867; TRANSPOSON-TN5563;
MEDLINE-20082846;
                                                                                                                                                                                                                                                                                                                                                                                                   4 EELNVPGEIVEXLXXXEESITR 25
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                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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                                                                                                                              SEQUENCE FROM N.A.
 F28H19.8 protein. F28H19.8.
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Length 334;

DB 10;

43.88;

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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006532; AAD20095.1; -.
InterPro; IPR001810; F-box.
                                                                 Pfam: PF00646; F-box; 1.
SMART: SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; 1.
SECURICE 334 AA: 37978 MW; 0D827279DD2EEF3F CRC64;
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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MEDLINE=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shean C.L., Barnstead M.E., Feldblyum T.V.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
          Gaps
                                                                                                                                                                                                                                                                                                          Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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EMBL, AP003592; BAB7498B.1; ..

Hypothetical protein; Complete protecome.

SEQUENCE 1299 AA: 141199 MW; FAE2808D4EED7C4C CRC64;
                                                                                                                                                                                                                                           Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
          9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Al13289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 AA.
                                                                                                                                   PRT; 1289 AA.
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           5; Mismatches
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                                                         161 ELESVRLSGDPLESLAGIDEIITR 184
                                       2 ELEELNVPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                                  Anabaena sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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              Conservative
                                                                                                                                       PRELIMINARY;
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Matches 9; Conserv
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                 10;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Varidiplantae; Streptophyta; Embryophyta; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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Methanobacterium thermoautotrophicum.
Archaea; Buryarchaeota; Methanobacteria; Methanobacterias.
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL589883; CAC34483.1; ...
Interpro; IPR01005; Myb_DNA_binding.
PROSITE; PS00037; MYB_L; UNKNOWN_1.
SEQUENCE 544 AA; 61940 MW; 4B5E73E2B9EB75CF CRC64;
                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heim S., Kunkel A., Thauer R.K., Hedderich R.; "Thiol:fumarate reductase (Tfr) from Methanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUNR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                          544 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.38; Score 45.5; 1
38.58; Pred. No. 47;
                                               8; Mismatches
Score 46;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 RENRRINTDGEAIDALFMATEEAVTR 36
                                                                                              1 RELEELNVPGEIVEXLXXX--EESITR 25
                                                                                                                          32 KEFEKIHIPNEIVEELLVRLPVKSLTR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RELEELNVPGEIVEXL-XXXEESITR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=98237600; Pubmed=9578488;
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                   DNA excision repair protein.
                               .0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                               Best Local Similarity 37.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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thermoautotrophicum Identification of the catalytic sites for fumarate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aldredge T., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Spadafora D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Jawani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski J., Reeve J.N., Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. S. Shimer G., Complete genome sequence of Methanobacterium thermoautotrophicum J. Beckeriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                        Ouery Match
42.9%; Score 45; DB 1; Length 488;
Best Local Similarity 61.5%; Pred. No. 50;
Matches 8; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                            488 AA; 53986 MW; 032EB355C4C8FEEA CRC64;
                                                -!- COFACTOR: BINDS A 2FE-28 CLUSTER (BY SIMILARITY).
EMBL, AJ000942; CAA04399.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OEF9554ED909C5DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Funazate reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492 AA.
                                                                                                                                             InterPro; IRR004017; DUF24.
InterPro; IPR004017; DUF24.
InterPro; IPR001041; Ferredoxin.
Pfam; PF02754; DUF224; 2.
Pfam; PF00111; fer2; 1.
TIGRFAMS; TIGR00384; dhsB; 1.
PROSITE; PS00197; ZFE28_FERREDOXIN; 1.
IIOn-sulfur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.9%; Score 45; DB
61.5%; Pred. No. 51;
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HSSP; P17596; 10LB.
InterPro; IPR0016564; ZFeZS_ferredoxin.
InterPro; IPR001450; 4FeXS_ferredoxin.
InterPro; IPR004489; DhsB.
InterPro; IPR001017; DUF224.
InterPro; IPR0010141; Ferredoxin.
                                                                             HSSP; P17596, 10LB.
InterPro; IPR000564; 2Fe2S_ferredoxin.
InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR004489; DhsB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00197; 2FE2S_FERREDOXIN; 1. PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanobacterium thermoautotrophicum.
                 reduction and thiol oxidation.";
Eur. J. Biochem. 253:292-299(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=DELTA H;
MEDLINE=98037514; PubMed=9371463;
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SEOUENCE 492 AA; 54780 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02754; DUF224; 2.
Pfam; PF00111; fer2; 1.
TIGRFAMS; TIGR00384; dhsB; 1.
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Length 492;

DB 17;

Best Local Similarity

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Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%; Score 45; DB 17; Length 587; 45.5%; Pred. No. 62;
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              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BRISTOL N2;
Blanchard M., Gattung S., Sansone J.;
"The sequence of C. elegans cosmid F52G3.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               587 AA; 68436 MW; B90DBC1E19C05E86 CRC64;
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 92.2 kba protein.
           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   807 AA.
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                                                                                                                                                                                                                                                                                             01-OCT-2001 (TrEMBLrel. 18, Created)
                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=21332296; Pubmed=11427726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                     BPS2 protein homolog (bps2).
                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 18, (TrEMBLrel. 20,
8; Conservative
                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sulfolobus solfataricus.
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                                                                                       205 KELNVPGDAIEKL 217
                                                       4 EELNVPGEIVEXL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=2287;
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01-MAR-2002
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Matches
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                Gaps
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Escherichia.
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44.4%; Pred. No. 2.1e+02;
tive 4; Mismatches 6; Indels (
                                                                                                        42.9%; Score 45; DB 5; Length 807; 45.0%; Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1752 AA; 191683 MW; 6182AC451D5BE1F8 CRC64;
                                                                                                                                  7; Indels
                                              Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. BMBL, AF026212; AAF99971.1; ... Hypothetical protein. SEQUENCE 807 AA; 92161 MW; 6919513906B0DB0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
conjugative transfer: oriT nicking-unwinding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1756 AA
                                                                                                                                                                                                                                           PRT; 1752 AA.
                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequent-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mature 413:852-856(2001).
EMBL; AE006471; AAL23509.1; -.
Plasmid; Complete Proteome.
                                                                                                                                                                           277 ELDELDVSGNVPDGLTAEEE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 44.4%;
8; Conservative
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                                                                                                                                                              2 ELEELNVPGEIVEXLXXXEE 21
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                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                Salmonella typhimurium.
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Best Local Similarity
                                 Waterston R.; "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                          Best_Local Similarity
Matches 9; Conserv
                   STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
[3]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                      Salmonella.
NCBI_TaxID=602;
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                                                                                                                 Query Match
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Q9WTB0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                           RESULT 13
Q93GL4
                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEGURAL FACATION M45;
SETRAIN=A3(2) / M445;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Harper D., Bateman A., Brown S., Hidalgo J., Hornsby T., Howarth S.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Seeger T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.4%; Score 44.5; DB 16; Length 284; 36.0%; Pred. No. 33; 1; Live 8; Mismatches 7; Indels 1;
  Sampei G., Mizobuchi K.; Sampei G., Mizobuchi K.; Tation of plasmid genomes: complete "Organization and diversification of Fre RIO0 genome", "incleotide sequence of Frhe RIO0 genome", "DDBJ databases. Submitted (MAY-1999) to the BMBL/GenBank/DDBJ databases. BMBL; AP000342; BAA78885.1; --
                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                           42.98; Score 45; DB 2; Length 1756; 44.48; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coelicolor A3(2).";

Nature 417:141-147(2002).

BMBL. A153861; CAB8881.1; -.

Hypothetical protein 30476 MW; A29B3E2E9E021D97 CRC64;

SEQUENCE 284 AA; 30476 MW;
                                                                                                                                                      1756 AA; 191683 MW; 56477ED2DC915BB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created) 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-0CT-2000 (TrEMBLrel. 21, Last annotation update) Hypothetical protein SC01385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 AA.
                                                                                                                                                                                                                                                                         4; Mismatches
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|961 VPGELMETLTSGORAATR 978
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                                                                                                                                                                                                                                                                                                                                 8 VPGEIVEXLXXXEESITR 25
                                                                                                                                                                                                                            Query Match
Best Local Similarity 44.44
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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SEQUENCE FROM N.A.
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
                                                                                                                                                                                                                           (without alignments)
91.669 Million cell updates/sec
                                                                                                                                                                                    February 11, 2003, 18:06:55 ; Search time 36.3402 Seconds
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                  1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \begin{array}{c} \operatorname{Minimum\ DB\ seq\ length:\ 0} \\ \operatorname{Maximum\ DB\ seq\ length:\ } 2000000000 \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	phosphopentide 4.	A# obi+accodenceda	FIIOSDIIOSE **	Anticariogenic pro	Casein phosphopept	phoenhonentide der	a contraction of the contraction	Sequence of Casetil	Sodium caseinate t	nos alpha-s2-casel	100 000 1111111111111111111111111111111	Phosphopeptide 14.	anying alpha-52 Ca	
	QI		AAP/1323	2 AAR14450	3 AAR28428	A AAR32930		4 AAR32311	5 AAR47817	6 AAR68939		19 AAW666U1	1 AAB12803	00000	B AAM32220
	Query Match Length DB		25 B	25 1	25 1	25.	7 1	25	25 1	25.			25	) !	222
æ	Query Match I		96.3	96.3	96		0.06	96.3	96.3		30.5	96.3	96		96.3
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(VICT-) VICTORIA DAIRY INDUSTRY AUTHORITY.

Bovine alpha-S2 ca Phosphopeptide 4.	Alpha-S2 casein pr	Capra hircus alpha	Alpha-S2 casein pr	Goat alpha-52 case	Sheep alpha-52 cas	Drosophila melanog	Drosophila melanog	Mouse ischaemic co	Human polypeptide	Arabidopsis thalia	Arabidopsis thalia	acti	Arabidopsis thalia	Arabidopsis thalia	A thaliana ribofl	Arabidonala mature	Arabidopsis ribofl	1000	+ 6401	Tates	+ + 4 9 1 1	2 0	-4 4	2 .	n (	Arabidopsis precui	'n	ຜ	<b>-</b> 1	SIS FIDOI	dopsis thali	dopsis thati	sis thali	Sison			
AAE17468																					<b>AAE2052</b>	AAG0523	AAG5004	AAG0523	AAG5004	AAY973	AAB0415	ABB7907		AAE2053	AAG4378	AAC4378	0701044	AAG4378	AAG3456	ALIGNMENTS	
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222	223	223	223	223	223	1077	1111	7141	007	4 0	יות מיני	197	181	200	200	202	208	208	208	208	208	270	270	271	271	271	271	271	271	271	279	0 7 0	7 (	320	209		
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Caries; gingivitis; periodontal disease; osteoporosis; osteomalacia.
                                                                                                                                                         /label= phosphoserine
                                                                                                                                                                         /label= phosphoserine
                                                                                                                          /label= phosphoserine
                                                                                                                                         /label= phosphoserine
                                                                                                        Location/Qualifiers
           AAP71323 standard; peptide; 25 AA.
                                                                                                                                                                                                                        87WO-AU00172.
                                                                                                                                                                                                                                       86AU-0006385
                                             07-MAY-1991 (first entry)
                                                             Phosphopeptide 4.
                                                                                                                                   Modified-site
                                                                                                                                                                   Modified-site
                                                                                                                   Modified-site
                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                         12-JUN-1986;
                                                                                                                                                                                          WO8707616-A.
                                                                                                                                                                                                          17-DEC-1987.
                                                                                              Synthetic
                              AAP71323;
RESULT 1
        AAP71323
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0
                                                             New phosphopeptides contg. defined aminoa cid sequence - useful in
treatment of dental, rarefying bone diseases and disease relating to
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                  caries; gingivitis; periodontal disease; osteoporosis; osteomalacia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel phosphopeptides - useful for treating dental diseases, rarefying diseases or diseases relating to malabsorption of minerals
                                                                                                                 The phosphopeptide is used in compsns. at a conc. of 0.01-5 wt8. See also AAP71320-P71324.
                                                                                                                                                                                       0
                                                                                                                                                               96.3%; Score 103; DB 8; Length 25; 84.0%; Pred. No. 7.1e-11; live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                Phosphopeptide #4 for increasing mineral absorption.
                                                                                                                                                                                                                                                                                                                                                                                                          'note= "phosphoserine (Pse)"
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                               1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                           AAR14450 standard; Protein; 25 AA.
 (UYME-) UNIVERSITY OF MELBOURNE
                                                                                               Claim 7; Page 17; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (VICT-) VICTORIAN DAIRY INDUSTRY.
                                                                                                                                                                                                                                                                                                                                                                                                /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                          /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Pse"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Pse"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Pse"
                                                                               malabsorption of minerals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90US-0563798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-0563798
                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                               21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYME-) UNIV OF MELBOURNE,
                                            WPI; 1987-362707/51.
          (REYN/) EC REYNOLDS.
                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-316875/43.
                                                                                                                                             25 AA;
                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                           Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                                                                                                                                                                                                                               10-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5015628-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1991
                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                              AAR14450;
                                                                                                                                                                               Matches
                                                                                                                                                                                                                                           RESULT 2
                                                                                                                                                                                                                                                     AAR14450
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This is an example of a highly generic formula for a phosphopeptide of length 5-13 amino acids. The peptides can be made synthetically (e.g. chemical synthesis or generic engineering) or they can be extracted from cereals, nuts or vegetables or by fractionating a digest of casein, alpha-s-casein, beta-casein or a salt of it. Compositions comprising the peptide may take the form of foodstuff to or confectionery, dentifrices; mouthwashes and preparations for significantly increase absorption of gingival tissue. The peptides the gut. See AAR14447-R14451.
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Casein; metal ion; dietectic; purification; growth medium; dietary supplement; fertiliser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The peptide may be prepd. by completely digesting casein in soln. with a proteolytic enzyme, adding mineral acid to the soln. to adjust the pH to 4.7, removing any precipitate, adding calcium
                                                                                                                                                                                                                                                                                               ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Selected phospho-peptide(s) prodn. having anticariogenic activities etc. - comprises digesting soluble monovalent cation salt of casein in soln., introducing di- or trivalent metal ion and filtering through filter having mol. wt. exclusion limit
                                                                                                                                                                                                                                                     Score 103; DB 12; Length 25;
Pred. No. 7.1e-11;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
Claim 1; Column 11; 8pp; English.
                                                                                                                                                                                                                                                                                                                 1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                             AAR28428 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 11; 18pp; English.
                                                                                                                                                                                                                                                   96.3%;
84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anticariogenic phosphopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92WO-AU00175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91AU-0005706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                   21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-382039/46.
                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                    25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                                                                                                                                                                                                                     Matches
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chloride to cause aggregation of the peptides in soln. and separating the aggregated phosphopeptides. This method allows prodn of the phosphopeptide by industrial methods. The phosphopeptide has anticariogenic activity and may be used as a dietectic. The peptide may be used in a microbiological growth medium, as a dietary supplement or as a fertiliser.
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Controlling dental calculus by treating teeth with oral compsns. - which contains phospho-peptide(s) having 5-40 amino-acyl
                                                                                                                                                                                                                                                                                                                                                                                                                   Casein; phosphopetide; dental calculus; salts; alkaline metal; alkaline earth metal; Zn/phosphopetide complex; aggregate; anti-caries; anti-gingivitis.
                                                                                                                                                                         ó;
                                                                                                                                            Score 103; DB 13; Length 25; Pred. No. 7.1e-11;
                                                                                                                                                                         4; Indels
                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 17; 23pp; English.
                                                                                                                                                                                                                          AAR32930 standard; Protein; 25 AA
                                                                                                                                                                                                        1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92WO-AU00441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-0748344
                                                                                                                                                  96.3%;
84.0%;
                                                                                                                                                                                                                                                                                                                                                                     02-JUL-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               Casein phosphopeptide #4.
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYME ) UNIV MELBOURNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1993-093685/11.
                                                                                           See also AAR28425-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gingivitis agents.
                                                                                                                                                                Best Local Similarity
Matches 21; Conserv
                                                                                                                           25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9303707-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          residues
                                                                                                                                                                                                                                                                                                                                           AAR32930;
                                                                                                                           Sequence
                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                    RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The peptide sequence is that of a phosphopeptide prepd. from a tryptic digest of casein. The peptide may be used with an anticalculus agent, e.g. alkali metal pyrophosphate, in a compsn. for controlling dental tartar. The compsn. inhibits conversion of brushite and amorphous calcium phosphate into the more stable hydroxyapatite on the teeth. The compsn. is used in the form of a mouthwash, toothpaste, gel, lozenge or chewing gum, for care of the teeth and tartar control.
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phospho-peptide(s) for dental tartar control - are included in compans, with pyrophosphate(s) or zinc salts to provide good
                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.3%; Score 103; DB 14; Length 25; 84.0%; Pred. No. 7.1e-11; 1.ve 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         /note= "post-translationally phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "post-translationally phosphorylated"
                                                                                                                                                                                                                                                                                                                                                         /note= "post-translationally phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                /note= "post-translationally phosphorylated"
                                                                                                                                                                                                                                                              Dental; teeth; tartar control; brushite; calcium phosphate;
               96.3%; Score 103; DB 14; Length 25; 84.0%; Pred. No. 7.1e-11; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                             nydroxyapatite; mouthwash; toothpaste.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 14; 17pp; English.
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                         Phosphopeptide derived from casein.
                                                                                                                                                                 AAR32311 standard; peptide; 25 AA.
                                                                      1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                          1 NANEEEYSIGSSEESAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91GB-0017315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92EP-0202024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Conservative
                                                                                                                                                                                                                   (first entry)
                                                21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See also AAR32308-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNIL ) UNILEVER PLC. (UNIL ) UNILEVER NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-060322/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 AA;
                         Query Match
Best Local Similarity
25 AA;
                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-1992;
                                                                                                                                                                                                                       10-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burger AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP528458-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                           AAR32311;
 Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                   Matches
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Duross JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW66601;
                                                                                                                                                                                                                                                                                                         hygiene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphopeptide; tryptic digestion; sodium caseinate; alpha(s1)-caseinate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                     Casein phosphopeptide; dentinal hypersensitivity; therapy; tooth.
                                                                                                                                                                                                                                                                                                                                                         Ser(P) = post-translationally phosphorylated serine. A mixture of casein phosphopeptides (CPP) and/or their salts may be used in a method for treating dentinal hypersensitivity. Pref. those CPPs contg. the sequence -Ser(P)-Ser(P)-Ser(P) - predominate. The CPPs can be extracted from a casein digest.
                                                                                                                                                                                                                                                                                                                   Treatment of dentinal hypersensitivity - using casein, component of casein, phospho-protein or phospho-peptide or their salts
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                             96.3%; Score 103; DB 15; Length 25; 84.0%; Pred. No. 7.1e-11; ive 0; Mismatches 4; Indels
                                                                                                                                                                       /label= Ser(P)
/note= "see also residues 16,17,18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sodium caseinate tryptic phosphopeptide T4.
                                                                                                       Sequence of casein phosphopeptide (CPP).
                                                                                                                                                                                                                                                                    (VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                         Location/Qualifiers
                                                       AAR47817 standard; peptide; 25 AA.
1 NANEEEYSIGXXXEEXAEVATEEVK 25
         Disclosure; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR68939 standard; Peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92AU-0003221.
                                                                                                                                                                                                                              93WO-AU00319.
                                                                                      21-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Conservative
                                                                                                                                                                                                                                                             UYME ) UNIV MELBOURNE
                                                                                                                                                                                                                                                                                                    WPI; 1994-025888/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            25 AA;
                                                                                                                                                             Modified-site
                                                                                                                                                                                                                            29-JUN-1993;
                                                                                                                                                                                             WO9400146-A.
                                                                                                                                                                                                             06-JAN-1994.
                                                                                                                                                                                                                                                                                     Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1995
                                                                                                                                       Synthetic.
                                                                        AAR47817;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR68939;
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                              AAR47817
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phosphoserine; phosphothreonine; phosphotyrosine; phosphohistidine; sugar; sorbitol; mannitol; xylitol; lactitol; cellobiitol; confectionary; carles; gingivitis; calcium; remineralisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides (AAR68936-40) are phosphopeptides resulting from the tryptic digestion of sodium caseinate. The peptide shown here is derived from the TCPK-tryptic digest of alpha(s2)-caseinate (comprising alpha(s2), alpha(s3), alpha(s4) and alpha(s6)). The peptides contain the amino phosphohistidine, and include in their sequence aspartate and glutamate. The phosphopeptides form part of a novel composition containing the peptide dispersed uniformly in a crystal mix of sugars chosen from sorbitol, mannitol, xylitol, lacticol, cellobiitol or mixtures of instead of conventional sugars to manufacture confectionary products. The phosphopeptides are known to inhibit caries and gludyitis and can act as a source of calcium ions to promote/enhance remineralisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crystalline poly:ol compositions for use in confectionery and pharmaceuticals - contain a phospho:peptide uniformly distributed within the crystal matrix and can improve oral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                               /note= "Phosphoserine"
                                                                                                                                                                                                                                                                                                                                                                                      "Phosphoserine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Phosphoserine"
                                                                                                                                                                                                                                                                                                       'note= "Phosphoserine"
                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; column 4; 8pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW66601 standard; peptide; 25 AA.
                                                                                                                                                                                                       /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                               /label= OTHER
                                                                                                                                                                                                                                                                                                                                                         /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                              /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94EP-0304083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.3%;
84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ICIL ) ICI AMERICAS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-044845/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 AA;
                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-1994.
                                                                                                     Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP629393-A.
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The compositions are useful in humans and in veterinary medicine in domestic animals such as cattle, sheep, horses and companion animals e.g. cats and dogs as well as zoo animals. The present sequence represents a phosphopeptide component of a specifically claimed complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a stable calcium phosphate complex including phosphopeptide stabilised amorphous calcium phosphate (ACP) or its derivative, where the phosphopeptide includes the amino acid sequence: Ser(P)-Ser(P)-Glu-Glu. The amorphous phases stabilised by the phosphopeptides are a delivery vehicle for co-localisation of Ca, Producing superior anticaries efficacy over prior art. The amorphous phases stabilised by the phosphopeptides are also useful as dietary supplements to increase calcium bioavallability and to help prevent supplements to increase calcium bioavallability and to help prevent diseases associated with calcium deficiencies. They are particularly useful for treatment or prevention of dental caries, calcium malabsorption and bone diseases such as osteoporosis and osteomalacia.
                                casein; calcium phosphate complex; amorphous calcium phosphate; ACP; phosphopeptide; delivery vehicle; calcium fluoride; calcium deficiency; osteoporosis; osteomalacia; tooth; bone disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stable calcium phosphate complex including phospho:peptide stabilised amorphous calcium phosphate - useful for treatment cdental caries, calcium malabsorption and bone diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.3%; Score 103; DB 19; Length 25; 84.0%; Pred. No. 7.1e-11; ive 0; Mismatches 4; Indels
     Bos alpha-s2-casein X-4P (f46-70) phosphopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 35; 43pp; English
                                                                                                                                                                                                                                                                                                 /note= "Ser(P)"
                                                                                                                                                                                             'note= "Ser(P)"
                                                                                                                                                                                                                                "Ser(P)"
                                                                                                                                                                                                                                                                'note= "Ser(P)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            osteoporosis and osteomalacia.
                                                                                                                                                                                                                                                                                                                                                                                                  98WO-AU00160.
                                                                                                                                                                                                                                                                                                                                                                                                                                       97AU-0005662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYME ) UNIV MELBOURNE
                                                                                                                                                                                                                                   /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-520803/44.
                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                      Modified-site
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                                                                                                                                                                                                                                                                                                                                       WO9840406-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                      17-SEP-1998
                                                                                                                                  Bos taurus.
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                                                                                                                 Synthetic.
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omprising a suspension or solution of a phosphopeptide (II) in water and thickening agent to form a thixotropic gel. (I) can have attinifiammatory and osteopathic activities. (I) can have attinifiammatory and osteopathic activities. (I) is useful for treating and preventing dental caries and dental sensitivity, gingivitis, mouth odour, osteoporosis, calculus formation in oral cavity in humans and animals. (I) is also useful for recrystallising and remineralising the enamel and/or dentine and also for buffering plaque against decrease in pH in humans and animals. Unlike prior art formulations, (I) has an pH in humans and is capable of producing a reliable gel without a loss of activity of (II) and other bloactive constituents. AAB12800 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protective peptide formulation for treating and preventing various dental disorders, gingivitis in humans and animals, has a suspension or solution of phosphopeptide in water and thickening agent to form a gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                 Phosphopeptide; protective peptide formulation; thixotropic gel; thickening agent; antimicrobial; antiinflammatory; osteopathic; dental caries; dental sensitivity; gingivitis; mouth odour; osteoporosis; calculus formation; oral cavity; recrystallising; remineralising; enamel; dentine; buffering plaque.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.3%; Score 103; DB 21; Length 25; 84.0%; Pred. No. 7.1e-11; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                     /note= "phosphoserine"
                                                                                                                                                                                                                                                                                                  "phosphoserine"
                                                                                                                                                                                                                                                                                                                              /note= "phosphoserine"
                                                                                                                                                                                                                                            /note= "phosphoserine"
                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 18; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PACI-) PACIFIC BIOLINK PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  99AU-0008135.
                                                                                                                                                                                                                                                                                                                                                                                                                      13-JAN-2000; 2000AU-0010070.
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                                   23-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-482993/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 AA;
                                                                   Phosphopeptide T4.
                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                               AU721548-B.
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                                                                                                                                                                                        Synthetic
         AAB12803;
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q
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RESULT 10 AAW32220

AAB12803 standard; peptide; 25 AA.

RESULT 9 AAB12803

1 NANEEEYSIGSSSEESAEVATEEVK 25

1 NANEEEYSIGXXXEEXAEVATEEVK 25

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Best Local Similarity 84.0 Matches 21; Conservative

Query Match

0; Gaps

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(PEPS-) PEPSYN LTD.
                                                                                     Smith JA;
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CONSTRUCTION OF STATE OF S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents bovine alpha-S2 casein precursor. Peptides having an amino acid sequence which is substantially identical to the C-terminal end of an alpha-S2 casein precursor, are used for manufacture of a medicament or foodstuff for promoting growth in humans
                                                                                                                                                    Bovine alpha-S2 casein precursor; growth promoting; mitogenic assay; platelet-derived growth factor; insulin-like derived growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manufacture of medicament or foodstuff for promoting growth - using peptide(s) with a sequence identical to the C-terminal end of an alpha-S2 casein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.3%; Score 103; DB 18; Length 222;
84.0%; Pred. No. 8.1e-10;
Live 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine alpha-S2 casein precursor protein,
  AAW32220 standard; protein; 222 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 3; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE17468 standard; Protein; 222 AA
                                                                                                                Bovine alpha-S2 casein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NANEEEYSIGSSSESAEVATEEVK 85
                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith JA, Wilkinson MC;
                                                                                                                                                                                                                                                                                                                               96WO-GB02658.
                                                                                                                                                                                                                                                                                                                                                                    95GB-0022302.
                                                                       03-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-2001; 2001WO-GB02601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000; 2000GB-0016189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       (UYLI-) UNIV LIVERPOOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-272048/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO20020133-A2.
                                                                                                                                                                                                                                                W09716460-A1
                                                                                                                                                                                                                                                                                                                           31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                31-OCT-1995;
                                                                                                                                                                                                                                                                                       09-MAY-1997.
                                                                                                                                                                                                               Bos taurus.
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                                        AAW32220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE17468;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
qq
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The invention relates to a composition comprising a peptide or its derivative. The peptide contains an amino acid sequence from alpha-S2 casein precursor. The peptides stimulate the growth of fibroblasts, and thus the synthesis and secretion of collagen. The peptides also stimulate of skin surface. The peptide is useful in the formation and regeneration in the form of a toothpasts or a chewing gum, for alleviating or preventing periodontal disease and a medicament preventing periodontal disease and a medicament in the form of a cosmetic composition for alleviating or preventing an effect of aging, particularly wrinkling of the skin. The present sequence is bovine alpha-S2 casein precursor protein.
                                                                     alpha-S2 casein precursor in the manufacture of a medicament for alleviating or preventing periodontal disease and an effect of aging in
                                             Use of peptide or its derivative containing an amino acid sequence in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphopeptide; active agent; oral; composition; anionic; polymeric; stabiliser; carboxylate; polymer; sulfonate; destabilisation; fluoride; caries; gingivitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.3%; Score 103; DB 23; Length 222; 84.0%; Pred. No. 8.1e-10; ive 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= Phosphoserine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label- Phosphoserine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 NANEEFYSIGXXXEEXAEVATEEVK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 6; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.50,
Best Local Similarity 84.08,
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Tys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92EP-0202023.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAY-1993 (first entry)
WPI; 2002-154690/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphopeptide 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Query Match
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                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                              RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of peptide or its derivative containing an amino acid sequence in alpha-S2 casein precursor in the manufacture of a medicament for alleviating or preventing periodontal disease and an effect of aging in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a composition comprising a peptide or its derivative. The peptide contains an amino acid sequence from alpha-S2
                                                                                                                                                                                                    anionic polymers were chosen from a group consisting of carboxylate polymers, sulfonate polymers, polymers having both a carboxylate and a sulfonate moiety, and other such mixtures. The anionic polymeric stabiliser inhibits destabilisation of the phosphopeptide in the oral environment. These oral compositions, pref. containing a fluoride source may be used for inhibiting caries and gingivitis.
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                 The sequences given in AAR31237-42 represent phosphopeptides which were used as the active agents in an oral composition. These peptides were stabilised by an anionic polymeric stabiliser. The
                                                                                        Oral compsns. contg. a phospho:peptide - with addn. of an anionic polymeric stabiliser to inhibit destabilisation in the oral
                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                     88.8%; Score 95; DB 14; Length 25; 80.0%; Pred. No. 1.7e-09; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha-S2 casein precursor (alpha-S2-CN) protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 8; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE17469 standard; Protein; 223 AA
                                                                                                                                              Disclosure; Page 16; 18pp; English.
                                             Schick LA;
                                                                                                                                                                                                                                                                                                                                                                           1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                          1 NANEEEXSIGSSSEESAEVATEEVK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 80.0
Matches 20; Conservative
                                               Elliott DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-154690/20.
                     (UNIL ) UNILEVER PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEPS-) PEPSYN LTD
                                                                      WPI; 1993-019802/03.
         (UNIL ) UNILEVER NV
                                                                                                                                                                                                                                                                                                     25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200202133-A2.
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                                                                                                                          environment
                                                Burger AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE17469;
                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
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The invention relates to a composition comprising a peptide or its derivative. The peptide contains an amino acid sequence from alpha-S2 casein precursor. The peptides stimulate the growth of fibroblasts, and the structure of the growth of fibroblasts, and secretion of collagen. The peptides also stimulate the growth of keratinocytes, which aid in the formation and regeneration of skin surface. The peptide is useful in the manufacture of a medicament in the form of a toothpasts or a chewing gum, for alleviating or preventing periodontal disease and a medicament in the form of a cosmetic composition for alleviating or preventing an effect of aging, particularly wrinking of the skin. The present sequence is goat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goat; alpha-S2 casein; dermatological; antiinflammatory; fibroblast; collagen; keratinocyte; skin regeneration; medicament; toothpaste; aging; chewing gum; cosmetic; wrinkling; periodontal disease.
                      thus the synthesis and secretion of collagen. The peptides also stimulate thus the synthesis and secretion of collagen. The peptides also stimulate growth of keratinocytes, which aid in the formation and regeneration of skin surface. The peptide is useful in the manufacture of a medicament in the form of a toothpaste or a chewing gum, for alleviating or a commenting periodontal disease and a medicament in the form of a cosmetic composition for alleviating or preventing an effect of aging, composition for alleviating of the skin. The present sequence is alpha-52 casein precursor (alpha-52-CN) protein.
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casein precursor. The peptides stimulate the growth of fibroblasts, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   82.2%; Score 88; DB 23; Length 223; 72.0%; Pred. No. 3.2e-07; Live 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capra hircus alpha-S2 casein C precursor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.2%; Score 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE17471 standard; Protein; 223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 NANEEEYSIRSSSEESAEVAPEEIK 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 72.03
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200202133-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE17471;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                  Alpha-S2 casein; alpha-S2-CN; dermatological; antiinflammatory; cosmetic; fibroblast; collagen; keratinocyte; skin regeneration; medicament; aging; toothpaste; chewing gum; cosmetic; wrinkling; periodontal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a composition comprising a peptide or its derivative. The peptide contains an amino acid sequence from alpha-S2 casein precursor. The peptides stimulate the growth of fibroblasts, and thus the synthesis and secretion of collagen. The peptides also stimulate of skin surface. The peptide is useful in the formation and regeneration in the form of a Lochtpaste or a chewing qum, for alleviating or preventing periodontal disease and a medicament in the form of a cosmetic composition for alleviating or preventing an effect of aging, particularly wrinkling of the skin. The present sequence is alpha-S2 casein precursor (alpha-S2-CN) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of peptide or its derivative containing an amino acid sequence in alpha-S2 casein precursor in the manufacture of a medicament for alleviating or preventing periodontal disease and an effect of aging in
                                  Gaps
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82.2%; Score 88; DB 23; Length 223;
Best Local Similarity 72.0%; Pred. No. 3.2e-07;
Matches 18; Conservative 1; Mismatches 6; Indels
                          6; Indels
                                                                                                                                                                                                                                                   Alpha-S2 casein precursor (alpha-S2-CN) protein #2.
    72.0%; Pred. No. 3.2e-07;
tive 1; Mismatches 6
                                                                                                                                                       AAE17475 standard; Protein; 223 AA.
                                              1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                Disclosure; Page 9; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUN-2001; 2001WO-GB02601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2000GB-0016189.
                                                                                                                                                                                                                     22-APR-2002 (first entry)
                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-154690/20.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEPS-) PEPSYN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 AA;
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                                                                                                                                                                                                                                                                                                                                                Unidentified.
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                                                                                                                                                                                        AAE17475;
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Search completed: February 11, 2003, 18:16:55 Job time : 37.3402 secs

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Sequence 2, Appli
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Sequence 4, Ap
Sequence 7, Ap
Sequence 7, Ap
Sequence 9, Ap
Sequence 11, A
Sequence 10, A
Sequence 10, A
Sequence 36, A
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                                                                                       (without alignments)
59.459 Million cell updates/sec
                                                                      February 11, 2003, 18:14:31; Search time 12.3711 Seconds
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                                                                                                                                                                                                                                                                                                                                                   Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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7: /cgn2_6/ptodata/1/iaa/pcaycomB.pep:*
7: /cgn2_6/ptodata/1/iaa/pcaycomB.pep:*
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               Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-748-344B-4
US-08-954-965A-4
US-08-137-086-4
US-09-1066-408-7
US-09-066-408-9
US-09-066-408-11
US-09-066-408-11
US-09-066-408-11
US-09-066-408-11
US-09-181-183-10
US-09-280-040-10
US-09-280-040-10
US-09-280-040-10
US-09-280-040-36
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US-08-961-083-120
US-09-360-545-6
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US-08-767-579-6
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compug
                                                                                                                                                                                                                262574 seqs, 29422922 residues
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                                                                                                                                                    1 NANEEEYSIGXXXEEXAEVATEEVK 25
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Listing first 45 summaries
                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Sequence 1, Appli Sequence 1, Appli Sequence 31, Appl Sequence 118, Appl Sequence 23, Appl Sequence 24, Appl Sequence 24, Appl Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli		
28 37 34.6 637 4 US-09-398-395A-58 29 37 34.6 686 3 US-09-224-024-31 31 37 34.6 686 3 US-09-224-024-31 32 37 34.6 686 5 PCT-US94-07902-31 33 37 34.6 1040 4 US-08-961-083-118 34 37 34.6 2089 1 US-08-418-893D-23 35 36 33.6 2089 1 US-08-418-893D-24 35 33.6 2089 1 US-08-418-893D-24 35 33.6 282 3 US-09-372-902-7 37 33.6 282 3 US-09-372-903-7 38 35.5 33.2 249 4 US-09-134-001C-4825 39 35.5 33.7 200 4 US-09-222-938A-40 41 35 32.7 200 4 US-09-282-938A-40 43 35 32.7 474 4 US-09-584-628-2 45 35 32.7 607 1 US-08-409-995-6	ALIGNMENTS	RESULT 1  US-07-748-344B-4  US-07-748-344B-4  Sequence 4, Application US/07748344B  Patent No. 5227154  GENERAL INPORMATION: FRINGLOS, ERIC CHARLES  TITLE OF INVENTION: PHOSPHOPEPTIDES FOR THE TITLE OF INVENTION: TREATMENT OF DENTAL CALCULUS  NUMBER OF SEQUENCES: 9  CORRESPONDENCE ANDRESS: 9  CORRESPONDENCE ANDRESS: 9  CORRESPONDENCE ANDRESS: 9  COUNTRY: USA  ZIP: MILMANUKE  STATE: MILMANUKE  COUNTRY: USA  ZIP: STATE: MISCONSIN  COUNTRY: USA  ZIP: STATE: PLOPPY DISK  COMPUTER READABLE FORM: MEDIUM TYPE: PLOPPY DISK  COMPUTER: IBM PC COMPATIBLE  COMPATIBLE  COMPUTER: IBM PC COMPATIBLE  COMPUTER: IBM PC COMPATIBLE  COMPUTER: IBM PC COMPATIBLE  COMPUTER: IBM PC COMPATIBLE  COMP
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Post-translationally phosphorylated serine

NAME/KEY: Phosphoserine LOCATION: 11

OTHER INFORMATION: OTHER INFORMATION:

TOPOLOGY: linear MOLECULE TYPE: Protein

FEATURE

NAME/KEY: Phosphoserine

FEATURE:

LOCATION: 13 OTHER INFORMATION: Post-translationally phosphorylated serine

NAME/KEY: Phosphoserine

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OTHER INFORMATION: POSt-translationally phosphorylated serine
                                                                                       LOCATION: 13 COTHER INFORMATION: POSt-translationally phosphorylated serine
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; OTHER INFORMATION: Post-translationally phosphorylated serine
US-07-748-3448-4
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                                                                                                                                                                                                                                                                                          Query Match 96.3%; Score 103; DB 1; Length 25; Best Local Similarity 84.0%; Pred. No. 8e-12; Matches 21; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: REYNOLDS, Eric Charles
TITLE OF INVENTION: A Treatment for Sensitive Teeth
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dental School, The University of Melbourne
CITY: Melbourne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/954,985A
FILING DATE: 21-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 28,922
REFENCE/DOCKET NUMBER: 322-00033
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 271-7590
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08954985A Patent No. 5981475 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,479
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: WOZNY, Thomas M
REGISTRATION NUMBER: 28,922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM
OPERATING SYSTEM: Windows 95
                                                                          NAME/KEY: Phosphoserine
                                                                                                                                                                        NAME/KEY: Phosphoserine
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Phosphoserine
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Australia
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CLASSIFICATION:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3000
                                                                                                                                                                                            LOCATION:
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LOCATION: 16

OTHER INFORMATION: Post-translationally phosphorylated serine

US-08-954-985A-4
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                                                                                                                                                                                                                                                                                                                                                   APPLICANT: REYNOLDS, ERIC CHARLES
TITLE OF INVENTION: PRODUCTION OF PHOSPHOPEPTIDES FROM CASEIN
NUMBER OF SEQUENCES:
OKRESPONDENCE ADDRESS:
ADDRESSEE: ANNHUS, SCEALES, STARKE & SAWALL
STREET: 100 EAST WISCONSIN AVE., SUITE 1100
CITY: MIWAUKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Post-translationally phosphorylated serine
                                                                                  96.3%; Score 103; DB 2; Length 25;
84.0%; Pred. No. 8e-12;
tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OUTTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,086
FILING DATE: 04-MAR-1994
CLASSIFFCATION: 530
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                       US-08-137-086-4; Sequence 4, Application US/08137086; Patent No. 6448374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: C.84
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-2022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (608) 255-2022
TELEFAX: (608) 255-2182
TELES: 26832 ANDSTARK
INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                Best Local Similarity 84.0
Matches 21, Conservative
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Gaps

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4; Indels

84.0%; Pred. No. le-10; tive 0; Mismatches

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1 NANEEEYSIGXXXEEXAEVATEEVK 25
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Best Local Similarity 84.0%
Matches 21; Conservative
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                                                                                                                                                                   RESULT 5
US-09-066-408-7
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                              Post-translationally phosphorylated serine
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APPLICANT: Wilkinson, Mark Charles
APPLICANT: Wilkinson, Mark Charles
APPLICANT: Wilkinson, Mark Charles
TITLE OF INVENTION: Casein Fragments Having Growth Promoting
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 12
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.3%; Score 103; DB 3; Length 222;
                                                                                                                                                                                           Query Match
96.3%; Score 103; DB 4; Length 25;
Best Local Similarity 84.0%; Pred. No. 8e-12;
Matches 21; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,408 FILING DATE: 13 MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 018317-000100US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB96/02658
FILING DATE: 31-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9522302.0
FILING DATE: 31-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                          1 NANEEEYSIGSSSEESAEVATEEVK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 6, Application US/09066408
; Patent No. 6060448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                             NAME/KEY: Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dow, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
               OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                  OTHER INFORMATION:
OTHER INFORMATION:
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US-09-066-408-6
                                                                                                   LOCATION
                                                                                                                                                            US-08-137-086-4
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Gaps
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Sequence 7, Application US/09066408; Sequence 7, Application US/09066408; Sequence 7, Application US/09066408; Sequence 7, Application US/09066408; Sequence 7, Applicant: Smith, John Arthur APPLICANT: Wilkinson, Mark Charles APPLICANT: Hui, Qing-Ming TITLE OF INVENTION: Casein Fragments Having Growth; TITLE OF INVENTION: Activity NUMBER OF SEQUENCES: 12 NUMBER OF SEQUENCES: 12; CORRESPONDENCE ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "goat alpha-S2 casein
precursor allele A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARACTION NUMBER: US/09/066,408
FILING DATE: 13-MAR-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB96/02658
FILING DATE: 31-OCT-1996
PRIOR APPLICATION NUMBER: GB 9523302.0
FILING DATE: 31-OCT-1995
APPLICATION NUMBER: GB 9522302.0
FILING DATE: 31-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                : Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 amino acids
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                       STREET: TWO band
CITY: San Francisco
France: California
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dow, Karen B.
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CYHER INFORMATION:
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Best Local Similarity
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Matches
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                                                          APPLICANT: Smith, John Arthur
APPLICANT: Smith, John Arthur
APPLICANT: Wilkinson, Mark Charles
APPLICANT: Liu, Qing-Ming
TITLE OF INVENTION: Casein Fragments Having Growth Promoting
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Smith, John Arthur
APPLICANT: Wilkinson, Mark Charles
APPLICANT: Wilkinson, Mark Charles
APPLICANT: Liu, Qing-Ming
TITLE OF INVENTION: Casein Fragments Having Growth Promoting
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,408
FILING DATE: 13-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1.223
OTHER INFORMATION: /note= "goat alpha-S2 casein
OTHER INFORMATION: precursor allele C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.2%; Score 88; DB 3; I
72.0%; Pred. No. 4.4e-08;
Live 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               018317-000100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB96/02658
FILING DATE: 31.0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9522302.0
FILING DATE: 31.0CT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
Sequence 9, Application US/09066408
Patent No. 6060448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 NANEEEYSIRSSSEESAEVAPEEIK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/POCKET NUMBER: 01831
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 8, Application US/09066408 ; Patent No. 6060448
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 72.09
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Protein
                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    94111-3834
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                                                                                                                                                                                                                                                                                                               COUNTRY:
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0; Gaps
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Patent No. 6060448
GENERAL INFORMATION:
APPLICANT: Smith, John Arthur
APPLICANT: Wilkinson, Mark Charles
APPLICANT: Liu, Qing-Ming
TITLE OF INVENTION: Caseln Fragments Having Growth Promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.5%; Score 84; DB 3; Length 223; 68.0%; Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 13-MAR-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "goat alpha-S2 casein
precursor allele B"
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Erancisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
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                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB96/02658
FILING DATE: 31-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9522302.0
FILING DATE: 31-0CT-1995
ATTORIEX/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER PR PR PROPEN FLOPPY
COMPUTER: PEN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 01833
TELECOMMUNICATION INFORMATION:
TELEFAN: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Dow, Karen B. REGISTRATION NUMBER: 29,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 223 amino acids
amino acid
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                                                                                             ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..223
OTHER INFORMATION:
OTHER INFORMATION:
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nes 17; Conserv
                                                                                USA
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                                                                              COUNTRY:
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302-992-8112

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TELEPHONE:
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                                                                                                                              TOPOLOGY:
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                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "sheep alpha-S2 casein
precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E. I. DU PONT DE NEMOURS AND COMPANY
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,408 FILING DATE: 13-MAR-1998 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: VIITANEN, PAUL VEIKKO
APPLICANT: BACOT, KAREN ONLEY
APPLICANT: JORDAN, DOUGLAS BRIAN
ITILE OF INVENTION: LUBAZINE SYNTHASE AND
ITILE OF INVENTION: RIBOFLAVIN SYNTHASE
                                                                                                                                                                                                                                                                   018317-000100US
                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB96/02658
FILING DATE: 31-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 952302.0
FILING DATE: 31-0CT-1995
ATTORNEY/ASTENTION:
NAME: DOW, KATEN B.
REGISTRATION NUMBER: 29,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: MICROSOFT WORD VERSION 7.0A CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/181,183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
RECISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL-1083
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: DISKETTE, 3.50 INCH
IBM PC COMPATIBLE
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Patent No. 6146866
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET UNMBER: 01831
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: E. I. DU PONT DE
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                      223 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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CTHER INFORMATION:

CTHER INFORMATION:

US-09-066-408-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-181-183-10
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                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                       Length 208;
                                                                                                                                                                                                                                                                                  9; Indels
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MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET CITY: WILMINGTON
                                                                                                                                                                                                                                         Ouery Match
41.1%; Score 44; DB 4;
Best Local Similarity 34.8%; Pred. No. 2.3;
Matches 8; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDIVIDUAL ISOLATE: Mature arabidposis RS
                                                                                                                                                                        ; INDIVIDUAL ISOLATE: Mature arabidposis RS US-09-181-183-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VIITANEN, PAUL VEIKKO
APPLICANT: BACOT, KAREN ONLEY
APPLICANT: DORDAN, DOUGLAS BRIAN
ITILE OF INVENTION: LUMAZINE SYNTHASE AND
ITILE OF INVENTION: RIBOFLAVIN SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: DELAWARE COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/280,040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: FLCYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL-1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09280040 Patent No. 6323013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 NEEEYSIGXXXEEXAEVATEEVK 25
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TELEPHONE: 302-992-8112
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                                                                                                   not relevant
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 10:
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Best Local Similarity 34.88
Matches 8; Conservative
                                                            I: 208 amino acids
amino acid
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                                                                                                                      not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 39
                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                      MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                   STRANDEDNESS:
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APPLICANT: VITTANEN, PAUL V.
APPLICANT: JORDAN, DAUGLAS B.
TITLE OF INVENTION: RIBOFLAVIN SYNTHASE GENES AND ENZYMES
TITLE OF INVENTION: RIBOFLAVIN SYNTHASE GENES AND ENZYMES;
TITLE OF INVENTION: AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/277,700
CURRENT FILING DATE: 1999-03-26
EARLIER PILING DATE: 1999-03-26
EARLIER PILING DATE: AUGUST 15, 1997
NUMBER OF SEQ ID NOS: 39
SOFTWARE: MICROSOft Office 97
SEQ ID NO 10
LENGTH: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.1%; Score 44; DB 4; Length 208; ilarity 34.8%; Pred. No. 2.3; Conservative 6; Mismatches 9; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95 SOFTWARE: MICROSOFT WORD VERSION 7.0A CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/181,183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.3; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: VIITANEN, PAUL VEIKKO
APPLICANT: VIITANEN, RAENO ONLEY
APPLICANT: JORDAN, DOUGLAS BRIAN
TITLE OF INVENTION: LUMAZINE SYNTHASE AND
TITLE OF INVENTION: REPOFLAVIN SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNITED STATES OF AMERICA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-8112
                                                                                                         Sequence 10, Application US/09277700 Patent No. 6350597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 36, Application US/09181183
Patent No. 6146866
  55 NAEEFTVGLAPETLRKTSLEELK 77
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55 NAEEFTVGLAPETLRKTSLEELK 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: arabidopsis
US-09-277-700-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: DELAWARE COUNTRY: UNITED
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                                                            RESULT 11
US-09-277-700-10
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US-09-181-183-36
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                                                                                                                                      Length 271;
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                                                                                                                                                                          Indels
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MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
APPLICATION DATA:
APPLICATION NUMBER: US/09/280,040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: E. I. DU PONT DE NEMOURS AND COMPANY 1007 MARKET STREET
                                                                                                                                                                        6
                 TOPOLOGY: not relevant
MOLEGULE TYPE: protein
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: arabidopsis RS precursor
                                                                                                                             Query Match 41.1%; Score 44; DB 4;
Best Local Similarity 34.8%; Pred, No. 3.1;
Matches 8; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: arabidopsis RS precursor
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VIITANEN, PAUL VEIKKO
APPLICANT: BACOT, KAREN ONLEY
APPLICANT: JORDAN, DOUGLAS BRIAN
TITLE OF INVENTION: LUMAZINE SYNTHASE AND
TITLE OF INVENTION: RIBOFLAVIN SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
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                                                                                                                                                                                                                                                                                                                                       ; Sequence 36, Application US/09280040 ; Patent No. 6323013
                                                                                                                                                                                                                                  118 NAEEFTVGLAPETLRKTSLEELK 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
RECISTRATION NUMBER: 33, CL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 302-992-8112
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INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 100, ______TY: WILMINGTON
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STRANDEDNESS: not
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Matches 8; Conserve
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STRANDEDNESS:
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                                                                                           US-09-181-183-36
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| Sequence 12, Application US/09066408
| GENERAL INFORMATION:
| APPLICANT: Smith, John Arthur
| APPLICANT: Wilkinson, Mark Charles
| APPLICANT: Liu, Oing-Ming
| TITLE OF INVENTION: Casein Fragments Having Growth Promoting
| TITLE OF INVENTION: Activity
| NUMBER OF SEQUENCES: 12
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Townsend and Townsend and Crew LLP
| STREET: Two Embarcadero Center, Bighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                41.1%; Score 44; DB 4; Length 271;
34.8%; Pred. No. 3.1;
tive 6; Mismatches 9; Indels
Patent NO. 6350597

GENERAL INFORMATION:
APPLICANT: VITANEN, PAUL V.
APPLICANT: BACTO, KAREN O.
APPLICANT: BORDAN, DOUGLAS B.
TITLE OF INVENTION: RIBOFLAVIN SYNTHASE GENES AND ENZYMES
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: CL-1083-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PILING DATE: 13-MAR-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 018317-000100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEPRAX: (415) 576-0300
INFORMATION FOR SED ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/277,700
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 08/912,218
EARLIER FILING DATE: AUGUST 15, 1997
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Microsoft Office 97
SOFTWARE: ALCOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB96/02658
FILING DATE: 31-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9522302.0
FILING DATE: 31-0CT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 NEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 34.8
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dow, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      California
                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: arabidopsis
US-09-277-700-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-066-408-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: S
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

NAME/KEY: Protein

COTHEN INFORMATION: precursor"

OTHEN INFORMATION: precursor"

OLEY MAICh

OLEY MAICh

SEST LOCAL 1.235

OURTY MATCh

ST.4%: Score 40: DB 3; Length 235:

OURTY MATCh

BEST LOCAL Similarity 32.0%: Pred. No. 13;

BEST LOCAL Similarity 32.0%: Pred. No. 13;

MATCHES 8; CONSERVATION 31: Nismatches 14; Indels

OY 1 NANEEEYSIGXXXEEXARVATEEVK 25

OY 1 NANEEEYSIGXXXEEXARVATEEVK 25

OY 1 NANEEEYSIGXXXEEXARVATEEVK 86

SEATCH COMPLETED FEBRUARY 86

SEATCH COMPLETED: PROTEIN 11, 2003, 18:22:09

JOB time: 13:5711 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                               OM protein - protein search, using sw model
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(without alignments) 52.729 Million cell updates/sec February 11, 2003, 18:19:51; Search time 12.1134 Seconds Run on:

1 NANEEEYSIGXXXEEXAEVATEEVK 25 US-09-380-738A-3 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

140259 Total number of hits satisfying chosen parameters:

140259 seqs, 25548876 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

Published_Applications_AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

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14: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 10,	Sequence 10, 1	Seguence 36, 1	-585B-36 Sequence 36, Appl	Sequence 32,	1-914-26 Sequence 26, Appl	Sequence 52,	Sequence 15,	US-09-986-552-15 Sequence 15, Appl	Sednence	Sequence 5	US-09-815-242-12123 Sequence 12123	US-09-815-242-12803 Sequence 12803		.2030	36	7	 	5-652-40 Sequence 40, App.
	ID	US-09-870-756-10	US-09-874	0S-09-870-756-36	US-09-874-585B-3	US-09-970-711-32	US-09-728-914-26	US-09-728-721-52	US-09-895-072-15	986-60-SN	US-09-815	US-09-815	US-09-815	US-09-815	US-09-815	US-09-815-242-1	US-09-895-913A-336	US-09-893-519A-4	US-09-819-104A-5	US-09-215-652-40
	DB	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	φ	6	σ	10
	Query Match Length	208	208	271	271	439	81	905	806	806	1226	246	246	246	246	103	191	587	2462	522
æ	Query Match	41.1	41.1	41.1	41.1	36.9	36.4	36.4	36.4	36.4	36.4	36.0	36.0	36.0	36.0	35.5	35.5	35.5	35.5	35.0
	Score	44	44	44	44	39.5	39	39	39	39	39	38.5	38.5	38.5	38.5	38	38	38	38	37.5
	Result No.		2	ורח	4	5	9	7	. 00	0	10	1	12	13	14	1.	16	17	18	19

Sequence 5802, Ap	Sednence 170, App	Sequence 24, Appl	58	Sequence 58, Appl	074	Sequence 118, App	Sequence 1340, Ap	•		19,		Sequence 68, Appl	Sequence 68, Appl.	Sequence 68, Appl	Sequence 68, Appl	Sequence 68, Appl	Seguence 68, Appl	Sequence 68, Appl	224	225	Sequence 226, App	Sequence 1, Appli	4	Sequence 23, Appl	Sequence 22, Appl	
US-09-738-626-5802	US-09-765-272-120	US-10-041-007-24	US-09-887-586A-58	US-09-903-012-58	US-09-815-242-10741	US-09-765-272-118	US-09-867-550-1340	US-09-764-868-805	US-10-136-253-7	US-10-012-140-19	US-09-841-786-4	US-10-028-072-68	US-10-121-049-68	US-10-123-904-68	US-10-140-470-68	US-10-175-746-68	US-10-176-918-68	US-10-176-921-68	US-09-771-161A-224	US-09-771-161A-225	US-09-771-161A-226	US-09-841-786-1	US-09-864-761-47710	US-10-023-528-23	119-09-788-657-22	
6	10	6	10	10	10	10	10	0	12	σ	10	6	5	6	6	6	σ	σ	10	10	10	10	10	12	10	1
103	522	637	637	637	730	1040	157	169	282	446	714	745	745	745	745	745	745	745	1175	1175	1175	3241	65	309	1360	TOOC
34.6	34.6	34.6	34.6	34.6	34.6	34.6	34.1	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.0	33.5		77.60
37	37	37	37	37	37	37	36.5	36	36	36	36	3 6	300	36	36	36	36	96	36	36	7	9 6	, , ,			33.0
20	21	22	23.0	24	25	26	27	. 60	568	0.00	3.5	3.5	3 6	34	3.0	36	37	30	0 6		-	- C V	9 6	7 7		4.0

## ALIGNMENTS

COMPOTER KENDELE FOR 3.50 INCH
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/870,756 CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET APPLICANT: VIITANEN, PAUL VEIKKO
BACOT, KAREN ONLEY
JORDAN, DOUGLAS BRIAN
TITLE OF INVENTION: LUMAZINE SYNTHASE AND
RIBOFLAVIN SYNTHASE COUNTRY: UNITED STATES OF AMERICA ZIP: 19898 REFERENCE/DOCKET NUMBER: CL-1083 NAME: FLOYD, LINDA AXAMETHY REGISTRATION NUMBER: 33,692 STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: protein ORIGINAL SOURCE: FILING DATE: 31-May-2001 CLASSIFICATION: <Unknown> TELECOMMUNICATION INFORMATION: sequence 10, Application US/09870756; Patent No. US20020052023A1; GENERAL INFORMATION: TELEPHONE: 302-992-8112 TELEFAX: 302-773-0164 LENGTH: 208 amino acids TYPE: amino acid ATTORNEY/AGENT INFORMATION: INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: COMPUTER READABLE FORM: CITY: WILMINGTON NUMBER OF SEQUENCES: STATE: DELAWARE US-09-870-756-10 RESULT 1

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RESULT 4
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APPLICANT: Jordan, Douglas Brain
APPLICANT: Bacot, Karen Onley
TITLE OF INVENTION: Riboflavin Synthase Genes and Enzymes and Methods of Use
CURRENT APPLICATION NUMBER: US/09/874,585B
CURRENT FILING DATE: 2002-03-05
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/874,585
PRIOR APPLICATION NUMBER: 08/912,218
PRIOR FILING DATE: 1997-08-15
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                                                                                 41.1%; Score 44; DB 10; Length 208; 34.8%; Pred. No. 1.9; Live 6; Mismatches 9; Indels
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
INDIVIDUAL ISOLATE: Mature arabidposis RS SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: VITTANEN, PAUL VEIKKO
BACOT, KAREN ONLEX
JORDAN, DOUGLESS BRIAN
TITLE OF INVENTION: LUMAZINE SYNTHASE AND
RIBOFLAVIN SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/870,756
                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09874585B
Patent No. US20020127670A1
GENERAL INFORMATION:
APPLICANT: Vlitanen, Paul Veikko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/09870756
Patent No. US20020052023A1
GENERAL INFORMATION:
                                                                                                                                                                3 NEEEYSIGXXXEEXAEVATEEVK 25
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55 NAEEFTVGLAPETLRKTSLEELK 77
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SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 208
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                                                                                                Local Similarity 34.88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 34.8 Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: arabidopsis
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                                                                                                                                                                                                                                                                RESULT 2
US-09-874-585B-10
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                                      US-09-870-756-10
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                                                                                     Query Match
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Matches
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APPLICANT: Vittanen, Paul Veikko
APPLICANT: Vittanen, Douglas Brain
APPLICANT: Jordan, Douglas Brain
APPLICANT: Bacot, Karen Onley
TITLE OF INVENTION: Riboflavin Synthase Genes and Enzymes and Methods of Use
FILE REFERENCE: CL1083 US DIV2
CURRENT APPLICATION WUMBER: US/09/874,585B
PRIOR APPLICATION NUMBER: 09/874,585
PRIOR APPLICATION NUMBER: 09/874,585
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 1997-08
RIOR FILING DATE: 1997-08
SOFTWARE: Microsoft Office 97
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APPLICANT: Chiocca, Susanna
APPLICANT: Kurzbauer, Robert
APPLICANT: Schaffner, Gotthold
TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
FILE REFERENCE: 0652.1800001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.1%; Score 44; DB 10; Length 271; 34.8%; Pred. No. 2.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE: arabidopsis RS precursor SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                   NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL-1083
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-8112
TELEPAX: 302-73-0164
INFORMATION FOR SEC ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 36, Application US/09874585B
; Patent No. US20020127670A1
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 NEEEYSIGXXXEEXAEVATEEVK 25
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Best Local Similarity 34.89
Matches 8; Conservative
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Best Local Similarity 34.8*
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Baker, Adam
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LENGTH: 271
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us-09-380-738a-3.rapb

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Sequence 15, Application US/09895072
Patent No. US2002002550A1
GENERAL INFORMATION:
APPLICANT: CANFIELD, WILLIAM M
TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLA
FILE REFERENCE: 2101199580CONT
CURRENT APPLICATION NUMBER: US/09/895,072
CURRENT FILING DATE: 2201-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CANFIELD, William PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROL TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROL FILE REFERENCE: 215089US77DIV CURRENT APPLICATION NUMBER: US/09/986,552 CURRENT FILING DATE: 2001-11-09
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Pred. No. 69;
                                                                                                                                                                                                                                                           36.4%; Score 39; DB 10; Length 905; 35.0%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURKENT FILING DATE: 2001-07-02

PRIOR APPLICATION NUMBER: 60/153,831

PRIOR FILING DATE: 1999-09-14

PRIOR APPLICATION NUMBER: US 09/635,872

PRIOR PILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PatentIn version 3.1

SEQ ID NO 15
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FASTEEQ for Windows Version 4.0
SEQ ID NO 52
LENGTH: 905
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PRIOR FILING DATE: 2000-08-10
PRIOR PELLING DATE: 2000-08-10
PRIOR PELLING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 155
LENGTH: 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/09986552
Patent No. US20020150981A1
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Best Local Similarity 43.5'
Matches 10; Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                         ) ORGANISM: Rattus rattus US-09-728-721-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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US-09-895-072-15
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; Sequence 26. Application US/09728914
; Sequence 26. Application US/09728914
; Patent No. US20010046499A1
; GENERAL INFORMATION:
; APPLICANT: FIKRIG. ERD.
; APPLICANT: PIKRIG. ERD.
; TITLE OF INVENTION: TICK ANTIGENS AND COMPOSITIONS AND METHODS COMPRISING; TITLE OF INVENTION: THEM
; TITLE OF INVENTION: THEM
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Best Local Similarity 39.1%; Pred. No. 4.7;
Matches 9; Conservative 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Position: 5366..6685/Product:IVa2 US-09-970-711-32
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CURRENT APPLICATION NUMBER: US/09/728,914
CURRENT FILING DATE: 2000-112-01
PRIOR PLILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 2000-10-16
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Vor: 2.1
                          CURRENT APPLICATION NUMBER: US/09/970,711
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/171,461
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIN Ver. 2.0
SOFTWARE: 439
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US-09-728-914-26
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Best Local Similarity 50.09
Matches 11; Conservative
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Ouery Match 36.4%; Score 39; DB 10; Length 908; Best Local Similarity 43.5%; Pred. No. 69; Matches 10; Conservative 3; Mismatches 6; Indels
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APPLICANT: Obleen, Kari L.
APPLICANT: Obleen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yu, H. Howard
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT FALLING DATE: 2001-03-21
PRIOR RPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/203
PRIOR APPLICATION NUMBER: 60/203,737
PRIOR PLILNG DATE: 2000-05-26
PRIOR PLILNG DATE: 2000-05-26
PRIOR PLILNG DATE: 2000-05-27
PRIOR PLILNG DATE: 2000-05-26
PRIOR PLILNG DATE: 2000-05-26
PRIOR PLILNG DATE: 2000-01-23
PRIOR PLILNG DATE: 2000-01-23
PRIOR PLILNG DATE: 2000-01-23
PRIOR PLILOR DATE: 2000-01-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                     Sequence 13646, Application US/09815242 Patent No. US20020061569A1
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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                                                                                                        1 NANEEFYSIGXXXEEXAEVATEE 23
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert
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Best Local Similarity 50.09
Matches 11; Conservative
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US-09-815-242-5461
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APPLICANT:
APPLICANT:
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Gaps
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General involvation:
General involvation:
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Yeskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yenamoto, Robert T.
TILLE OF INVENTION: Identification of Essential Genes in TILLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR APPLICATION NUMBER: 60/201,078
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/202,779
PRIOR PILING DATE: 2000-01-23
PRIOR PILING DATE: 2000-01-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-23
PRIOR PILING DATE: 2000-12-22
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                       FILE REFERENCE: ELLTRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEC ID NOS: 14110
SCOTWARE: PASLESEQ FOR WINGOWS VERSION 4.0
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36.0%; Score 38.5; D
Best Local Similarity 36.0%; Pred. No. 20;
Matches 9; Conservative 4; Mismatches
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| SEGYNVAVNYAGSKEKAEAVVEEIK 50
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Staphylococcus aureus
US-09-815-242-5461
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US-09-815-242-12123
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LENGTH: 246
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Length 246;
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR RILING DATE: 2000-03-21
PRIOR RILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,931
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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36.0%; Pred. No. 20;
tive 4; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12030
LENGTH: 103
                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                          CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 12030, Application US/09815242; Patent No. US20020061569A1; GENERAL INFORMATION:
                                                                                            CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELILING DATE: 2000-03-21
PRIOR PELILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR PELING DATE: 2000-10-27
PRIOR PELING DATE: 2000-10-27
PRIOR PELING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT; ORGANISM: Staphylococcus aureus; US-09-815-242-13100
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Yamamoto, Robert T.
Xu, H. Howard
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                  TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, Robert
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Best Local Similarity 30...
Best Similarity 30...
Secondary 30...
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US-09-815-242-12030
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APPLICANT:
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                                                                          36.0%; Score 38.5; DB 10; Length 246; 36.0%; Pred. No. 20;
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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Best Local Similarity 36.0%; Pred. No. 20;
Matches 9; Conservative 4; Mismatches
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-105-26
PRIOR FILING DATE: 2000-105-26
PRIOR FILING DATE: 2000-10-26
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
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Patent No. US20020061569A1
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Carr, Grant J.
Yamamoto, Robert T.
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Zyskind, Judith W.
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Carr, Grant J.
Yamamoto, Robert T.
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Zyskind, Judith W.
Wall, Daniel
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APPLICANT: Haselbeck, Robert
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                                                                                                             Best_Local Similarity 36.0 Matches 9; Conservative
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LENGTH: 246
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Gaps 3;

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; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-12030
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Ouery Match 35.5%; Score 38; DB 10; Length 103; Best Local Similarity 43.5%; Pred. No. 9.2; Matches 10; Conservative 2; Mismatches 11; Indels 0; Gaps

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2 ANEBEYSIGXXXEEXAEVATEEV 24 || || || || || || || 42 42 ANGEDVKIGLPVVEGAKVTAEVV 64

Search completed: February 11, 2003, 18:36:15 Job time: 13.1134 secs

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93.903 Million cell updates/sec
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                        US-09-380-738A-3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 4, Appli	Sequence 3, Appli	Sequence 40191, A	Sequence 39826, A	Sequence 30853, A	Sequence 140550,
SUMMARIES		QI	3 US-07-731-592B-4	US-09-380-738A-3	US-09-614-150-40191	US-60-191-637-39826	US-60-191-681-30853	US-09-791-537-140550
		DB	m	17	20	27	27	21
		Query Match Length DB ID	25	25	1277	1277	1277	137
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		Score		66	0,10	, r	20.50	4 8
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99-791-537- 50-173-464- 50-173-464- 50-191-637- 50-191-637- 50-191-637- 50-191-637- 50-791-637- 50-791-537- 50-791-537- 50-791-537- 60-791-537- 60-791-537- 60-791-537- 60-791-537- 60-791-537-	0.5.09.791.537.14234 0.5.09.791.537.142243 0.5.09.791.537.142246 0.5.09.791.537.142246 0.5.09.791.537.142287 0.5.09.791.537.142287 0.5.09.791.537.142309 0.5.09.791.537.142313 0.5.09.791.537.142313 0.5.09.791.537.142313 0.5.09.791.537.142343 0.5.09.791.537.142344 0.5.09.791.537.142344 0.5.09.791.537.142345 0.5.09.791.537.142345 0.5.09.791.537.142345 0.5.09.791.537.142345 0.5.09.791.537.142345 0.5.09.791.537.142345 0.5.09.791.537.142345 0.5.09.791.537.142345 0.5.09.791.537.142345 0.5.09.791.537.142345 0.5.09.791.537.142345	ALIGNMENTS 592B positions Containing a peptide ant, Unilever United Sta	5 inch, 1.44 Mb storage (R) 7/731,592B
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a nncc	595 596 737 738 748 758 766 775 777 777 777 777 777 777	ication Usurion: TION: Urger, Al. Ullott, ba TION: ONTION: ONTION: URTION: PADRESS Patent D River Ro, Watter 'Jersey	ABLE FORM: I: Diskette: I: Disk
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	44444444444444444446666666666666666666	4 Applications ORMANTON: Burger Burger Burger INVENTION INVENTION ORDER BES BES BES BES BES BAT	PUTER READABLE FO BLUM TYPE: Disk BLUM TYPE: Disk OMPUTER TYPE: DISK PERATING SYSTEM: OFTWARE: MICROSO OFTWARE: MICROSO DELICATION NUMBER LASSIFICATION: DATE: 1991 MURINE CRRACTERIS
44444 00000 44444444444 LUUUNUU0000000000000	44444444444444444444444444444444444444	SEULT 1 Sequence 4, Application Sequence 4, Application GENERAL INFORMATION: APPLICANT: Burger, A APPLICANT: BLIGLT, APPLICANT: BLIGLT, APPLICANT: BLIGLT, APPLICANT: CHICK, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE FOR SEQUENCES: CORRESPONDENCE ADDRESSED: ADDRESSED: Patent STREET: 45 RIVER GITY: Edgewater CITY: Edgewater COUTY: USA	COMPUTER READABLE FO MEDIUM TYPE: DISK COMPUTER: TYPE: DISK OPERATING SYSTEM: SOFTWARE: MICTOSO CURRENT APPLICATION APPLICATION NUMBER FILING DATE: 1991 CLASSIFICATION: 5 CLASSIFICATION: 5 INFORMATION: 5 SPOURNCE CHARACTERIE
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                                                                                                                    OTHER INFORMATION: Post-translationally phosphorylated OTHER INFORMATION: serine
                                                                                                                                                                                                                           Post-translationally phosphorylated serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 25;
                                                                                                                                                                                                                                                                                                                              Post-translationally phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Post-translationally phosphorylated; OTHER INFORMATION: serine US-07-731-5928-4
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92.5%; Score 99; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: RETVOLLDS, Eric
TITLE OF INVENTION: CALCIUM PHOSPHOPEPTIDE COMPLEXES
FILE REFERENCE: 040268/0161
CURRENT APPLICATION NUMBER: US/09/380,738A
CURRENT FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-03-13
PRIOR APPLICATION NUMBER: AU PO5562
PRIOR FILING DATE: 1998-03-13
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGH: 25
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LOCATION: (12). (12)
OTHER INFORMATION: Xaa is a phosphorylated Serine
LOCATION: (13)..(13)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
96.3%; Score 103; DB 3;
Best Local Similarity 84.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 4;
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OTHER INFORMATION: Xaa is a phosphorylated Serine
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US-09-380-738A-3
; Sequence 3, Application US/09380738A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     serine
                                                                                                                                                                                NAME/KEY: Phosphoserine
                                                                      NAME/KEY: Phosphoserine
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                     Unknown
                                                                                                                                                                                                                      OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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                                      Unknown
AMINO ACID
                 STRANDEDNESS:
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                                      TOPOLOGY:
                                                                                                  LOCATION:
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ATTLICANT. TO THE STATE OF INVESTIGATION OF THE STATE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: 06/15/832
PRIOR TILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-2-28
PRIOR FILING DATE: 1999-11-2-8
PRIOR FILING DATE: 2000-01-2-8
PRIOR FILING DATE: 2000-01-2-8
PRIOR FILING DATE: 2000-03-23
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GENERAL INFORMATION:
APPLICANT: Verter, J. Craig
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO00392
CURRENT APPLICATION NUMBER: US/60/191,637
CURRENT FILING DATE: 2000-03-23
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47.6%; Pred. No. 48;
Live 4; Mismatches 7; Indels 0
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47.6%; Pred. No. 48;
tive 4; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40191
LENGTH: 1277
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SOFTWARE: FastSEQ for Windows Version 4.0
                           Sequence 40191, Application US/09614150 GENERAL INFORMATION:
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                                                                               APPLICANT: Venter, J. Craig
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Matches 10; Conservative
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US-60-191-637-39826
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Matches 10; Conserv
US-09-614-150-40191
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2 ANEEEYSIGXXXEEXAEVATE 22

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1 NANEEEYSIGXXXEEXAEVATEEVK 25

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APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
ACID Sequences, Systems Containin the Nucleic Acid Sequences
TITLE OF INVENTION: and Uses Thereof
TITLE OF INVENTION: and Uses Thereof
TITLE OF INVENTION: and Uses Thereof
CURRENT APPLICATION NUMBER: US/60/161,932
CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 2626
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2609
LENGTH: 764
                                                                                                                                                                                                                                                                                                                                        Sequence 18812.
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50.0%; Pred. No. 1e+02;
tive 1; Mismatches 9; Indels 3:
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                                                                                                                                                     43.9%; Score 47; DB 21; Length 1280;
40.9%; Pred. No. 1.6e+02;
tive 6; Mismatches 7; Indels (
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                                                                                 ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-791-537-137326
               SOFTWARE: Patentin version 3.0
SEQ ID NO 137326
LENGTH: 1280
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NUMBER OF SEQ ID NOS: 153055
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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US-60-161-932-2609
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THRRE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THERE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERBNOE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                APPLICANT: LI, Peter, W.D.
APPLICANT: LI, Peter, W.D.
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
TITLE OF INVENTION: USES THEREOF.
FILE REPERBENCE: 0.1000390
CURRENT PRILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 30973
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47.6%; Pred. No. 48;
tive 4; Mismatches 7; Indels (
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FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 140550, Application US/09791537; GENERAL INFORMATION:
, APPLICANT: Bionomix, Inc.
                                                                                                                                   ; Sequence 30853, Application US/60191681
; GENERAL INFORMATION:
; APPLICANT: Li, Peter, W.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Arabidopsis thaliana
                   207 ADEDDXDYGDDDEEVAEPSTE 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Matches 9; Conserv
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US-09-791-537-140550
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                                                                                                       RESULT 5
US-60-191-681-30853
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SEQ ID NO 30853
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APPLICANY: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: US/09/614,150
CURRENT APPLICATION NUMBER: 60/157,832
PRIOR PILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-2
PRIOR FILING DATE: 2000-01-2
PRIOR FILING DATE: 2000-01-2
PRIOR FILING DATE: 2000-01-2
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEO ID NOS: 43008
SOFTWARE: FastESE for Windows Version 4.0
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TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000392
CURRENT APPLICATION UNBER: US/60/191,637
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 42660
SEQ ID NO 22940
SEQ ID NO 22940
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                    Sequence 22860, Application US/09614150 GENERAL INFORMATION:
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; Sequence 22940, Application US/60191637
; GENERAL INFORMATION:
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                                                                    APPLICANT: Venter, J. Craig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.09
Matches 13; Conservative
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ORGANISM: DROSOPHILA
US-09-614-150-22860
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LENGTH: 1417
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY A
            Sequence 18089, Application US/60191681
GENERAL INFORMATION:
TATALE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
TITLE OF INVENTION: USES THEREOF.
FILLE REFERENCE: C1000390
CURRENT APPLICATION NUMBER: US/60/191,681
CURRENT APPLICATION NUMBER: US/60/191,681
CURRENT BATE: 2000-03-23
NUMBER OF SEQ ID NOS: 30973
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CHEN, Xianford APPLICANT: CHEN, Xianford APPLICANT: CHEN, Xianford APPLICANT: SUBRAMANIAN, Gopalakrishnan APPLICANT: ZHENG, Liansheng TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS 84-89, 91-99 FILE REFERENCE: 2750-694P CURRENT APPLICATION NUMBER: US/09/497,191
CURRENT FILING DATE: 2000-02-03
SUFTANE: PATENT OF SEQ ID NOS: 920
SOFTWARE: PATENT VEF. 2.1
SEQ ID NO 756
LENGTH: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                      43.5%; Score 46.5; DB 27; Length 1417; 50.0%; Pred. No. 2.3e+02; tive 1; Mismatches 9; Indels 3;
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50.0%; Pred. No. 2.4e+02;
tive 1; Mismatches 9;
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FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12245, Application US/09791537 GENERAL INFORMATION:
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; GENERAL INFORMATION:
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ALEXANDROV, Nickolai
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 50.0°
Matches 13; Conservative
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Best Local Similarity 50.0%
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: DROSOPHILA
US-60-191-681-18089
US-60-191-681-18089
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                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SHAW, KAREN J.
APPLICANT: SHAW, KAREN J.
APPLICANT: SHAMEN TR., GEORGE H.
APPLICANT: SESTER, MARCO
APPLICANT: GENERAL JORK
APPLICANT: GREBNE, JONATHAN R.
ITLE OF INVENTION: ASPERGILLUS FUMIGATUS NUCLEIC ACIDS AND POLYPEPTIDES,
TITLE OF INVENTION: ASPERGILLUS FUMIGATUS NUCLEIC ACIDS AND POLYPEPTIDES,
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 2976-4020051
CURRENT APPLICATION NUMBER: 0200-09-29
PRIOR TILING DATE: 1990-09-29
PRIOR FILING DATE: 1990-09-29
NUMBER: OF SEQ ID NOS: 13925
SEQ ID NO 10079
LENGTH: 179
                                                                                                                                                                              0; Gaps
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43.0%; Score 46; DB 20; Length 179;
Best Local Similarity 34.8%; Pred. No. 18;
Matches 8; Conservative 5; Mismatches 10; Indels
                                                                                                                        Ouery Match
Best Local Similarity 36.0%; Pred. No. 13; Length 139;
Matches 9; Conservative 3; Mismatches 13; Indels
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                                                     ; FEATURE:
; OTHER INFORMATION: any n or Xaa = unknown
; OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 10079, Application US/09675784A; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT ; ORGANISM: Aspergillus fumigatus US-09-675-784A-10079
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-09-675-784A-10079
                                                FEATURE:
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Sequence 15, Appl
Sequence 4560, Ap
Sequence 92233, A
Sequence 92228, A
Sequence 92233, A
Sequence 92233, A
Sequence 76998, A
Sequence 76998, A
Sequence 76999, A
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Sequence 24, Appl
Sequence 24, Appl
Sequence 62, Appl
Sequence 5, Appli
Sequence 5, Appli
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9, Appli
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Sequence 618, App
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                                                                                                        (without alignments)
72.734 Million cell updates/sec
                                                                                      February 11, 2003, 18:17:56 ; Search time 28.6082 Seconds
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1. /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

2. /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

4. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-217-939-24

PCT - USO2 - 36122 - 62

US-09-782-110-5

US-10-950-084-6839

US-10-295-891-52

US-10-305-686-15

US-10-305-686-15

US-10-306-686-15

US-09-950-084-4560

US-09-950-084-4560

US-09-724-676-92228

US-09-724-676-92228

US-09-724-676-9223

US-09-724-676-9223

US-09-724-676-7699

US-09-724-676-7699
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                                                                                                                                                                                                                                                             420401 seqs, 83231269 residues
                                                                                                                                                                                     1 NANEEEYSIGXXXEEXAEVATEEVK 25
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                                                                                                                                                                                                                                                                                                                                                                                                   Listing first 45 summaries
                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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107
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Match Length DB
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No.
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Sequence 10, Appl Sequence 92227, A Sequence 92237, A Sequence 92237, A Sequence 76994, A Sequence 77004, A Sequence 77004, A Sequence 77004, A Sequence 77005, A Sequence 77005, A Sequence 77005, A Sequence 77005, A Sequence 77009, A		USE THEREOF	Length 779; ; Indels 0; Gaps		
5 US-09-636-458-10 5 US-09-724-676-92227 5 US-09-724-676-92232 5 US-09-724-676-92232 5 US-09-724-676-9944 5 US-09-724-676-76994 5 US-09-724-676-76994 5 US-09-724-676-77004 5 US-09-724-676-77004 5 US-09-724-676-77005 5 US-09-724-676-77005 5 US-09-724-676-77005 5 US-09-724-676-77005 5 US-09-724-676-77005 5 US-09-724-676-77009 5 US-09-724-676-77009 5 US-09-724-676-77009 6 US-09-724-676-77008 6 US-09-724-676-77008	ALIGNMENTS	PROTEINS AND	Score 46; DB 6; Pred. No. 9; 2; Mismatches 9	EV 24 	S/10310154 el D
35.5 35.5 35.5 35.5 35.5 35.5 35.5 35.5		ULT 1 10-222-851-28 sequence 28, Application US/10222851 seneral INFORMATION: APPLICANT: Hitachi LTD. APPLICANT: Hitachi LTD. TITLE OF INVENTYON: RP42-INTERACTING FILE REFERENCE: H0100926A1 CURRENT APPLICATION NUMBER: US/10/222 CURRENT FILING DATE: 2002-12-19 NUMBER OF SEQ ID NOS: 61 SOFTWARE: Patentin version 3.1 SEQ ID NO 28 LENGTH: 779 TYPE: PRT ONGANISM: HOMO SAPIENS -10-222-851-28	th 43.0%; Similarity 47.6%; 10; Conservative	EEEYSIGXXXEEXAEVATEEV 	SULT 2 Sequence 618, Application US/1031015, Sequence 618, Application US/1031015, Sequence 618, Application US/1031015, APPLICANT: Edgerton, Michael D APPLICANT: Chomet, Paul S. APPLICANT: Adams, Thomas H APPLICANT: Ruff, Thomas G. APPLICANT: Ball, James A. APPLICANT: Ball, James A. APPLICANT: Ball, Erin APPLICANT: Boduy G. APPLICANT: Boduy G. APPLICANT: Boduy Jinzho APPLICANT: Dong, Molian APPLICANT: Dong, Molian APPLICANT: Hinchey, Estephen M. APPLICANT: Hinchey, Brenda S. APPLICANT: Galligan, Meghan M. APPLICANT: Johnson, G. Richard APPLICANT: Johnson, G. Richard APPLICANT: Johnson, G. Richard APPLICANT: Johnson, G. Richard APPLICANT: Jung, Vincent
227 229 229 330 331 331 332 338 338 338 338 440 441 442 443 338 443 338 443 338 344 443 344 443 344 443 344 344		RESULT 1 US-10-222-851-28 Sequence 28, Application GENERAL INFORMATION: APPLICANT: Hitachi LTD. TITLE OF INVENTION: RP42; FILE REFERENCE: H0100928; CURRENT APPLICATION NUME: CURRENT FILING DATE: 2 NUMBER OF SEQ ID NOS: 61 SEQ ID NO 28 LENGTH: 779 TYPE: PRT TYPE: PRT US-10-222-881-28	Query Match Best Local S Matches 10	Qy 4 EEEY       Db 316 EEEE	RESULT 2 US-10-310-154- Sequence 618 GENERAL INFO APPLICANT: APPLI
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Appli Appli

Sequence 4

Sequence 11, Appl Sequence 2, Appli

us-09-380-738a-3.rapn

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104 EEEFNIQMAEEKAQKIATVE 123
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PCT-US02-36122-62
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LENGTH: 137
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US-09-782-130-5
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SEGUENCE 24, Application PC/TUS025586
APPLICANT BASE PLANT SCIENCE GMBH
TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS III
FILE REFERENCE: 16313-0156
CURRENT APPLICATION NUMBER: PCT/US02/25586
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/311,414
NUMBER OF SEQ ID NOS: 67
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TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REPERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR APPLICATION NUMBER: 60/337,358
NUMBER: OF SEQ ID NOS: 736
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40.2%; Score 43; DB 6; Length 1286;
Best Local Similarity 55.0%; Pred. No. 52;
Matches 11; Conservative 0; Mismatches 9; Indels
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40.0%; Pred. No. 12;
tive 5; Mismatches 7; Indels
                                                                                                                                                                                    McKiel, Christine L.
Miller, Philip W.
Padmavathi, Manchikanti
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Start, William G.
                     Lucille B.
                                                                                                                                                    Madson, Linda L.
Malloy, Kathleen A.
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Kretzmer, Keith A
                                                                                                                  Luethy, Michael M.
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ORGANISM: Arabidopsis thaliana
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                                   Lai, Chao-Qiang
                                                                                                                                                                                                                                                                                                                                                         Yang, Chunzhi
Zeng, Xiaoping
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SEQ ID NO 24
LENGTH: 137
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Matches 8; Conservative
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Zhao, Yajuan
Zhou, Li
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Wang, Haiyun
Xin, Zhanguo
Xu, Nanfei
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                                                                  Jie-Yi
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PCT-US02-25586-24
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Sequence 24, Application US/10217939
GENERAL INFORMATION:
GAPLICANT: MITTENDORF, VOLKER
APPLICANT: HERTEL, HEIKO A.
TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS III
FILLE REPERENCE: 16313-0157
CURRENT APPLICATION NUMBER: US/10/217,939
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/311,414
PRIOR APPLICATION NUMBER: 60/311,414
PRIOR PLILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN Ver. 2.1
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APPLICANT: KNAUE, VIC C.
APPLICANT: KRIDL, JEAN C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATED TRANSCRIPTION
TITLE OF INVENTION: AND EXPRESSION OF HETEROLOGOUS GENES
FILE REFERENCE: 16518.052
CURRENT APPLICATION NUMBER: US/09/782,130
CURRENT PILING DATE: 2001-02-12
PRIOR FILING DATE: 1999-01-15
PRIOR FILING DATE: 1999-01-15
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TITLE OF INVENTION: Alloiococcus Otitidis Infectious Disease Targets
FILE REFERENCE: Application 1
CURRENT APPLICATION NUMBER: PCT/US02/36122
CURRENT FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 106
SOFTWARE: Patentin version 3.1
SEQ ID NO 62
LENGTH: 369
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Best Local Similarity 38.18; Pred. No. 39;
Matches 8; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 62, Application PC/TUS0236122
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5, Application US/09782130 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana US-10-217-939-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Alloiococcus otitidis
PCT-USO2-36122-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 EEEVALAKRIEEGDEIAKQEL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 EEEFNIQMAEEKAQKIATVE 123
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRAN. TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRAN. FITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPERIENCE: 50661200122
CURRENT APPLICATION NUMBER: US 40/296,764
PRIOR PILING DATE: 2002-10-20
PRIOR PAPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR PILING DATE: 2001-10-22
PRIOR PILING DATE: 2001-0-31
PRIOR FILING DATE: 2002-04-34
NUMBER OF SEQ ID NOS: 9966
                                                                                       APPLICANT: George H. Shimer, Jr.
APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
APPLICANT: Roberta J. Shaw
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
FILE REFERENCE: 1034/10953US2
                                                                                                                                                                                                                                                                     FILE REFERENCE: 1034/1C963US2
CURRENT PAPLICATION NUMBER: US/09/950,084
CURRENT APPLICATION NUMBER: US 09/417,811
PRIOR FILING DATE: 1999-10-14
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR PELING DATE: 1999-03-10
PRIOR PELING DATE: 1999-03-10
PRIOR PELING DATE: 1999-03-10
PRIOR PELING DATE: 1999-03-11
PRIOR PELING DATE: 1999-03-16
PRIOR PELING DATE: 1998-03-16
PRIOR PELING DATE: 1998-03-16
PRIOR PELING DATE: 1998-03-16
PRIOR PELING DATE: 1998-03-06
PRIOR PELING DATE: 1998-03-06
PRIOR PELING DATE: 1998-03-06
PRIOR PELING DATE: 1998-03-06
PRIOR APPLICATION NUMBER: US 09/036,720
PRIOR PELING DATE: 1998-03-06
PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.4%; Score 39; DB 5; Length 643; 36.8%; Pred. No. 1.18+02; tive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 9358, Application US/10325899
; GENERAL INFORMATION:
                                           Sequence 6839, Application US/09950084 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Staphylococcus aureus US-09-950-084-6839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543 EEEHOLNADVEEQVEIOTK 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 EEEYSIGXXXEEXAEVATE 22
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APPLICANT: Ly, Ngoc
APPLICANT: Woodward, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 7; Conserva
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LENGTH: 830
                                 US-09-950-084-6839
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                                        PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1996-06-07
PRIOR FILING DATE: 1990-05-21
PRIOR PLICATION NUMBER: US 07/526,123
PRIOR PLICATION NUMBER: US 06/692,605
PRIOR APPLICATION NUMBER: US 06/692,605
PRIOR PILING DATE: 1986-10-17
PRIOR PILING DATE: 1990-09-14
PRIOR FILING DATE: 1990-09-14
PRIOR PILING DATE: 1988-04-29
PRIOR PILING DATE: 1988-04-29
PRIOR PILING DATE: 1988-04-29
PRIOR PILING DATE: 1988-04-36
PRIOR FILING DATE: 1988-04-36
PRIOR FILING DATE: 1988-03-15
PRIOR FILING DATE: 1988-03-15
PRIOR FILING DATE: 1988-03-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN VET. 2.1
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illarity 41.7%; Pred. No. 84;
Conservative 2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.4%; Score 39; DB 5; Length 134; 40.0%; Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TUD. THILLAN, Jennifer L.
APPLICANT: TANG, Y. TOM
APPLICANT: TANG, Y. TOM
APPLICANT: BAUGHN, MATIAA R.
APPLICANT: BAUGHN, MATIAA R.
APPLICANT: LU, DYUNG AIDA
APPLICANT: AZIMAZAI, Yalda
TITILE OF INVENTION: HUMAN HYDROLYTIC ENZYMES
TITILE REFERENCE: PF-0738 USN
CURRENT APPLICATION NUMBER: US/10/070,634A
CURRENT FILING DATE: 2002-10-25
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 28
SOFFWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 2458536CD1
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PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: US 08/484,941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 EEEYSIGXXXEEXAEVATEE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Brassica campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 10; Conserva
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Best Local Similarity
Matches 8; Conserv
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APPLICANT: CANTIELD, WILLIAM
TITLE OF INVENTION: PHOSHODIESTER ALPHA-GLCNACASE OF THE LYSOSOMAL TARGETING PAT
FILE REFERENCE: 23039702701V
CURRENT APPLICATION NUMBER: US/10/306,686
PRIOR PTLING DATE: 2002-11-29
PRIOR PTLING DATE: 2000-08-10
PRIOR FILING DATE: 1999-08-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATCHTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: George H. Snimer, Jr.
APPLICANT: George H. Miller
APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
APPLICANT: Roberta S. Hare
APPLICANT: Roberta S. Hare
APPLICANT: Roberta S. Hare
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
CURRENT APPLICATION NUMBER: US/09/950,084
PRIOR PELLING DATE: 1999-109-10
PRIOR PILLING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/366,557
PRIOR FILLING DATE: 1999-03-11
PRIOR PILLING DATE: 1999-03-11
PRIOR FILLING DATE: 1999-03-11
PRIOR FILLING DATE: 1999-03-11
PRIOR FILLING DATE: 1999-03-11
PRIOR FILLING DATE: 1999-03-10
PRIOR FILLING DATE: 1999-03-11
PRIOR FILLING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/036,538
PRIOR FILLING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/036,338
PRIOR FILLING DATE: 1999-03-10
PRIOR PELLING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/036,338
PRIOR FILLING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/036,338
PRIOR FILLING DATE: 1999-03-10
PRIOR FILLING DATE: 1999-03-10
PRIOR PELLING DATE: 1999-03-10
PRIOR FILLING DATE: 1999-03-10
PRIOR PELLING DATE: 1999-03-10
PRIOR PRIOR PELLING DATE: 1999-03-10
PRIOR PELLING DATE: 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.4%; Score 39; DB 6; Length 908 43.5%; Pred. No. 1.7e+02; tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 4560, Application US/09950084; GENERAL INFORMATION:
                                                                                                                                                          US-10-306-686-15; Sequence 15, Application US/10306686; GENERAL INFORMATION:
                                                 620 NANDEEFKI----QIAVEVDTRE 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  620 NANDEEFKI----QIAVEVDTRE 638
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ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: George H. Shimer, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 43.58
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mus musculus
US-10-306-686-15
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PRIOR APPLICATION NUMBER: US/09/340,620

PRIOR FILING DATE: 1999-06-28

PRIOR PELLOR DATE: 1999-06-20

PRIOR PELLOR OF THE CARD NUMBER: US/09/207,359

PRIOR PELLOR FILING DATE: 1998-10-08

PRIOR PELLOR FILING DATE: 1998-06-17

PRIOR PELLOR APPLICATION NUMBER: US/09/099,041

PRIOR PELLOR APPLICATION NUMBER: US/09/019,942

PRIOR PELLOR DATE: 1998-06-17

PRIOR PELLOR DATE: 1998-06-17

PRIOR PELLOR DATE: 1998-06-17

NUMBER OF SEQ ID NOS: 71

SOFTWARE: FASELEQ FOR WINDOWS VERSION 4.0
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TITLE OF INVENTION: METHODS OF PRODUCING HIGH MANNOSE GLYCOPROTEINS IN COMPLEX CARBOR
TITLE OF INVENTION: DEFICIENT CELLS
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                        36.4%; Score 39; DB 6; Length 830; 39.1%; Pred. No. 1.5e+02; tive 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.4%; Score 39; DB 6; Length 905; 35.0%; Pred. No. 1.6e+02; tive 6; Mismatches 7; Indels
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36.4%; Score 39; DB 1; Length 908;
Best Local Similarity 43.5%; Pred. No. 1.7e+02;
Matches 10; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: PCT/US02/37618
CURRENT FILING DATE: 2002-12-19
SUFUMBER PS EQ ID NOS: 21
SOFTWARE: PATENTIN VERSION 3 1
                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-10-295-981-52
Sequence 52, Application US/10295981
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               690 SSDEEKAGGLDDEEEAELVPSEV 712
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GENERAL INFORMATION:
                                                                                                                                                                                                                                 2 ANEEEYSIGXXXEEXAEVATEEV 24
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                                                                                                                                 Best Local Similarity 39.19
Matches 9; Conservative
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Best Local Similarity 35.v.
7; Conservative
                           , ORGANISM: Homo sapiens US-10-325-899-9358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Rattus rattus US-10-295-981-52
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ORGANISM: Mus musculus
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TYPE: PRT
                                                                                                                     Query Match
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US-09-950-084-4560

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8; Indels 10; Gaps
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                                                     Gaps
                                                     3;
Query Match
Best Local Similarity 36.0%; Score 38.5; DB 5; Length 166;
Best Local Similarity 36.0%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 35.5%; Score 38; DB 5; Length 212;
Best Local Similarity 35.5%; Pred. No. 45;
Matches 11; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 35.5%; Score 38; DB 5; Length 212;
Best Local Similarity 35.5%; Pred. No. 45;
Matches 11; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOCTWARE: Patentin version 3.2
SEQ ID NO 92233
LEMOTH: 212
                                                                                                                                                                                                                                                                                                             APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOGTWARE: PatentIn version 3.2
SEQ ID NO 9228
LENGTH: 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 92233, Application US/09724676 GENERAL INFORMATION:
                                                                                                                                                                                                                                              US-09-724-676-92228

US-09-724-676-92228, Application US/09724676

; GENERAL INFORMATION:
                                                                                                       4 EEEYSIG---XXXEEXAEVATEEVK 25
                                                                                                                                        ORGANISM: Homo sapiens
US-09-724-676-92233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-92228
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US-09-724-676-92233
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments) 109.706 Million cell updates/sec February 11, 2003, 18:14:11 ; Search time 21.9072 Seconds Run on:

US-09-380-738A-3 Title: Perfect score:

1 NANEEEYSIGXXXEEXAEVATEEVK 25 Sequence: 283224 seqs, 96134422 residues

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		- 1	caseın	-casein	w.	ч	lycerol K	kinase (	kinase (	kinase (	protein kinase (EC	cyclin-dependent k	protein kinase - c	probable riboflavi	CHS5 protein - yea		hypothetical prote	•	ď	TENTE T	VIIGI MAMO CICARIO	micro grucamic act	nypounerical proce	neurolilament proc	meralloprocernase	probable membrane	probable late embr	conserved hypothet	a)	hypothetical prote		
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B72421 T49019 S60675 S60675 QFPGL F75191 F75191 F31102 S63267 S63267 A81370 T31104 T61125 T71040
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### ALIGNMENTS

	RESULT 1
	alpha-s2-casein precursor - bovine
	C; Species: Bos primigenius taurus (cattle)
	C; Date: 01-Sep-1981 #sequence_revision 03-rep_1994 #text
	C; Accession: JQ2008; A29087; A91438; S66626; A03107
	R;Groenen, M.A.M.; Dijkhot, R.J.M.; Verstege, A.J.M.; van der 1001,
_	Gene 123, 187-193, 1993
	A; Title: The complete sequence of the gene encoaling boying argument construction.
_	A;Reference number: JQ2008; MUID:93154583; PMID:8428030
_	A; Accession: JQ2008
	A;Status: translation not shown
_	A; Molecule type: DNA
_	A; Residues: 1-222 <gro></gro>
	A:Cross-references: GB:M94327
_	R.Stewart, A.F.; Bonsing, J.; Beattie, C.W.; Shan, F.; Willis, I.:.;
_	Mol. Biol. Evol. 4, 231-241, 1987
_	A:Title: Complete nucleotide sequences of bovine alpha-sz and beta castar
_	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

ONAS: C A; Molecule type: mRNA A; Residues: 1-222 <STE> A; Cross references: GB:M16644; NID:g162928; PIDN:AAA30479.1; PID:g162929 A; Cross references: GB:M16644; NID:g162928; PIDN:AAA30479.1; PID:g162929 R; Brignon, G.; Ribadeau Dumas, B.; Mercier, J.C.; Pelissier, J.P.; Das, B.C. FBBS Lett. 76, 274-279, 1977 A, Reference number: A93062; MUID:88188989; A, Accession: A29087 A; Status: translation not shown

A;Molecule type: protein A;Residues: 16-101,'EE',104-222 <BRI> A;Residues: 16-101,'EE', previously designated s2, s3, s4, and s6, appear to have t A;Note: four fractions, previously designated s2, s3, s4, and s6, appear to have t Aritie: Complete amino acid sequence of bovine alpha-S2-casein. A; A; Reference number: A91438; MUID:77185633; PMID:862906 A; Contents: A allele A; Accession: A91438

Ricrosclaude, F.; Joudrier, P.; Mahe, M.F.

Ricrosclaude, F.; Joudrier, P.; Mahe, M.F.

J. Dairy Res. 46, 211-213, 1979

A.Fitle: A genetic and biochemical analysis of a polymorphism of bovine alpha-s2-c

A.Fotheres: annotation; D allele

A.Contents: annotation; D allele has a deletion of nine residues, which may be

R. Mote: the sequence of the D allele has a deletion of nine residues, which may be

R. Mote: the sequence of the D allele has a deletion of nine residues, which may be

R. Mote: the sequence of the D allele has a deletion of nine residues, which may be

R. Mote: the sequence of the D allele has a deletion of nine residues, which may be

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R. Mote: the sequence of the D allele has a deletion of nine residues.

R. Mote: the sequence of the D allele has a deletion of nine residues.

R. Mote: the sequence of the D al

A,Molecule type: protein A,Residues: 165-203 <2UC> C,Comment: The sequence of the A allele is shown.

C;Genetics:

A;Gene: alphas2ca A;Map position: 6 A;Introns: 17/3; 26/3; 33/3; 47/3; 56/3; 65/3; 74/3; 82/3; 97/3; 138/3; 147/3; 156

Gaps

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Indels

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1; Mismatches
                                                                                                        1 NANEEEYSIGXXXEEXAEVATEEVK 25
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                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 1-223 <BOU>
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                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Bouniol, C
                                               Matches
                                                                                                                                                                                                                                                                      RESULT 4
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C; Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 22-Jun-1999
C; Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 22-Jun-1999
C; Accession: A25070; S17856
Biochimie 67, 1043-1051, 1985
A; Hitle: Complete sequence of ovine alpha-s2-casein messenger RNA.
A; Reference number: A25070; MUID:86104467; PMID:3002499
A; Molecule type: mRNA
A; Mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: 146995
R; Bouniol, C.; Brignon, G.; Mahe, M.F.; Printz, C.
Anim. Genet. 25, 173-177, 1994
A; Tille: Blochemical and genetic analysis of variant C of caprine alpha s2-casein (Capra A; Reference number: 146995; MUID:95030556; PMID:7943951
A; Accession: 146995
                                                            F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-222/Product: alpha-s2-casein #status experimental <WAT>
F;23,24,25,31,71,72,73,76,144,146,158/Binding site: phosphate (Ser) (covalent) #status
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A:Residues: 1-93, 'T', 95-223 <BO2>
C:Superfamily: alpha-s2-casein
C:Keywords: mammary gland, milk; phosphoprotein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-223/Product: alpha-s2-casein #status predicted <KA2>
F:23, 24, 25, 32, 55, 72, 73, 74, 77, 145, 147, 159/Binding site: phosphate (Ser) (covalent) #statu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha s2-casein C - goat
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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C;Superfamily: alpha-s2-casein
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                                                                                                                                                                                                                                                                                4; Indels
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Pred. No. 1.4e-07;
G. Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A. Status: preliminary; translated from GB/EMBL/DDBJ
                              C: Keywords: mammary gland; milk; phosphoprotein
                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                     1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                61 NANEEEYSIGSSEESAEVATEEVK 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 NANEEEYSIRSSSEESAEVAPEEIK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                      96.3%;
84.0%;
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72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-s2-casein precursor - sheep
C; Superfamily: alpha-s2-casein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.5%;
72.0%;
                                                                                                                                                                                                                                                               21; Conservative
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                                                                                                                                                                                            Query Match
Best Local Similarity
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A; Residues: 1-223 <BOU>
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Matches 18; Conserv
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alpha-s2-casein precursor - goat
C;Species: Capra aegagrus hircus (domestic goat)
C;Decies: Capra aegagrus hircus (domestic goat)
C;Date: 31-Dec-1993 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: S33881, S33880, JNOS47; S20620
R;Bouniol, C.; Brignon, G.; Mahe, M.F.; Printz, C.
Protein Seq. Data Anal. 5, 213-218, 1993
A):Title: Characterization of goat allelic alphas2-caseins A and B: further evidence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K; yourloat, c. 235-236, 1993
A; Title: Sequence of the goat alpha-s2-casein-encoding CDNA.
A; Reference number: JN0547; MUID: 93216130; PMID: 8462880
A; Accession: JN0547
A; Ac
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C;Species; Arabidopsis thaliana (mouse-ear cress)
C;Species; Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G96796
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alocansen, N.F.; Hughes, B.; Huizar, L.
Conway, A.B.; Conway, A.B.; Conway, T.H.; Dewar,
Nature 408, 816-820, 2000
C,A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Khaykin, E.; Kim
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Southwick, A.M.; Sun, H.; Tall,
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Southwick, A.M.; Sun, H.; Tall,
A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1280 <STO>
A; Cross-references: GB:AE005173; NID:g6143896; PIDN:AAF04442.1; GSPDB:GN00141
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A.Note: allele B
A.Rocession: 33880
A.Molecule type: protein
A.Residues: 16-78, 'E', 80-223 <BO2>
A.Note: sequence deduced from compositional analysis of peptides
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protein kinase (EC 2.7.1.37) cdc2-related PITSLRE alpha 2-2 - human protein kinase cdc2-related PITSLRE alpha 2-4 (Contains: protein kinase cdc2-related PITSLRE alpha 2-4 (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 19-Dec-1997 (Species 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 19-Dec-1997 (Species 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 19-Dec-1997 (Species 21-Jul-1995 #sequence_revision 269, 15786-15794, 1994 (Species 21-Jul-1995 #sequence number: A54024; MujD:94253170; PMID:8195233 A; Accession: B54024 (MujD:94253170; PMID:8195233 A; Accession: preliminary; not compared with conceptual translation
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A; Status: preliminary: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 339-777
A; Residues: 339-777
A; Coss-references: GB:U04819
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases
C; Keywords: alternative splicing; ATP; phosphotransferase
F; 418-673/Domain: protein kinase homology <KIN>
F; 426-434/Region: protein kinase ATP-binding motif
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     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; not compared with conceptual translation
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Pred. No. 9.8;
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     Indels
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6
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          Mismatches
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             5
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                                                                                                      305 BEEEFTGSNSEFASEOSAEEV 325
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                                                          4 EEEYSIGXXXEEXAEVATEEV
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Best Local Similarity 47.6%
Matches 10; Conservative
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A;Cross-references: GB:U04818
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             10; Conservative
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A; Residues: 1-777 <XIA>
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A; Residues: 1-777 <XIA>
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                  Matches
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A; Note: authors translated the codon AAG for residue 5 as Leu, GAC for residue 6 as Lys, CTC for residue 351 as Phe, GAT for residue 418 as Glu, AAC for residue 457 as Lys, GTA C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo; Keywords: alternative splicing; ATP; phosphotransferase
C; Reywords: alternative splicing; ATP; phosphotransferase
F; 409-664/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: authors translated the codon AAA for residue 5 as Leu, GAC for residue 6 as Lys. CTC for residue 342 as Phe, CTG for residue 574 as Gln, AAG for residue 614 as Asn, GAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: Ti3709
R; Masai, I.; Okazaki, A.; Hosoya, T.; Hotta, Y.
R; Masai, I.; Okazaki, A.; Hosoya, T.; Hotta, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 11157-11161, 1993
A; Title: Drosophila retinal degeneration A gene encodes an eye-specific diacylglycerol A; Reference number: 217702; MUID:94068563; PMID:8248222
A; Accession: Ti3709
A; Accession: Ti3709
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                                                                                                                                                                                                                                                                                                                                                                                            diacylglycerol kinase (EC 2.7.1.107) - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 13-Aug_1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
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                                                                                                                         Score 47; DB 2; Length 1280;
Pred. No. 11;
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Pred. No. 16;
1; Mismatches
                                                                                                                                                                              6; Mismatches
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A;Cross-references: FlyBase:FBgn0003217
                                                                                                                                                                                                                                                                               36 DDDEYSIGTELSEESKVEEEKV 57
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50.0%;
                                                                                                                              43.9%;
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                                                                                                                                                                                      Conservative
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A; Residues: 1-1454 <MAS>
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A; Residues: 1-768 < XIA>
                                                                                                                                                         Best Local Similarity
Matches 9; Conserv
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                                                            A; Gene: F28016.18
                                                                                       A; Map position: 1
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                                          C; Genetics:
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4 EEEYSIGXXXEEXAEVATEEV 24

Length 768;

DB 2;

43.0%; Score 46; DB 2 47.6%; Pred. No. 9.6;

Query Match Best Local Similarity

Gaps

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9; Indels

Length 772;

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A:Introns: 37/3; 76/2; 118/1; 164/2; 208/1; 249/1; 283/1; 329/1; 351/1; 407/3; 438/
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase h
C;Keywords: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Arabidopsis thaliana Gnaun [amported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C; Accession: B86592
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C; Accession: B86592
M; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shan, M.; VanAken, S.E.; Umayam, L.; Tallor euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vente A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Accession: B84592
A; Accession: B84592
A; Accession: B8450; MUID: 20083487; PMID: 10617197
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-197 <STO>
A; Cross-references: GB: AE002093; NID: 94454479; PIDN: AAD20926.1; GSPDB: GN00139
A; Cenetics:
                                      A;Molecule type: DNA A;Residues: 1-772 <LIX>A;Residues: 1-772 <LIX>A;Cross-references: EMBL:U16656; NID:9571458; PIDN:AAA67037.1; PID:9571460
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                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                               42.1%; Score 45; DB 2;
47.6%; Pred. No. 14;
tive 2; Mismatches
                                                                                                                                                                                                                         F;413-668/Domain: protein kinase homology <KIN>F;421-429/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 2
C;Superfamily: riboflavin synthase alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 NEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                   311 EEEEETGSNSEEVSEQSAEEV 331
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                                                                                                                                    A; Gene: CPITSLRE
                                                                                                               C;Genetics:
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                                                                                                                      Cypecies: Homo sapiens (man)
Cybecies: Homo sapiens (man)
Cybecies: 10-101-1995 #sequence_revision 21-Jul-1995 #text_change 19-Dec-1997
CyAccession: E54024
Rixiang, J.; Lahti, J.W.; Grenet, J.; Easton, J.; Kidd, V.J.
J. Biol. Chem. 269, 15786-15794, 1994
Ayritle: Molecular cloning and expression of alternatively spliced PITSLRE protein kinas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Cross-references: GB:004824
C.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold
C.Seywords: alternative splicing; ATP; phosphotransferase
F:420-675/Domain: protein kinase homology <KIN>
F:428-436/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ril, H.; Grenet, J.; Valentine, M.; Lahti, J.M.; Kidd, V.J.
Gene 153, 237-242, 1995
A;Title: Structure and expression of chicken protein kinase PITSLRE-encoding genes.
A;Reference number: I50463; MUID:95180725; PMID:7875595
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C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
C:Accession: I50463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 9.8;
2; Mismatches 9; Indels
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Pred. No. 9.8;
2; Mismatches
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47.6%; Pred. No.
114 EEEEETGSNSEEASEQSAEEV 334
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47.68;
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Best Local Similarity
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A:Cross-references: EMBL:U20618; NID:92258165; PIDN:AAB64526.1; PID:9662142; GSPDB:GN
A:Experimental source: strain S288C (AB972)
CHSS protein - yeast (Saccharomyces cerevisiae)
N.Alternate names: protein LB543.18; protein YLR330w
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S53407
                                                                                                                                                                       R,Du, Z. submitted to the EMBL Data Library, February 1995 A;Description: The sequence of S. cerevisiae cosmid 8543. A;Reference number: $53390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: SGD:CHS5; CHS5; CAL3; MIPS:YLR330w
A;Cross-references: SGD:S0004322
A;Map position: 12R
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Gaps

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RESULT 15
S09659
hypothetical protein A3 - Rhizobium sp. insertion sequence ISR1
hypothetical protein A3 - Rhizobium sp. insertion sequence ISR1
C;Speciaes: Rhizobium sp.
C;Speciaes: Rhizobium sp.
C;Speciaes: Rhizobium sp.
C;Accession: S09659
R;Priefer, U.B.; Kalinowski, J.; Rueger, B.; Heumann, W.; Puehler, A.
Plasmid 21, 120-128, 1989
A;Title: ISR1, a transposable DNA sequence resident in Rhizobium class IV strains, shows
A;Reference number: S09659; MUID:89297222; PMID:2544911
A;Reference number: S09659
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-88 < PRI>
A;Cross-references: EMBL:X06616; NID:948670; PIDN:CAA29830.1; PID:948671
C;Genetics:
A;Mobile element: insertion sequence ISR1
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Query Match

41.1%; Score 44; DB 2; Length 671;
Best Local Similarity 55.0%; Pred No. 18;
Matches 11; Conservative 0; Mismatches 9; Indels
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278 NEEELSYSKENEPVAEVADE 297
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GenCore version 5.1.3

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2003, 18:07:35; search time 11.0825 Seconds

Title: US-09-380-738A-3

Perfect score: 107

Sequence: 1 NANBEEYSIGXXXEEXAEVATEEVK 25

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum Match 0%

Post-processing: Minimum Match 100%

Listing first 45 summaries
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SwissProt_40:*

Database :

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O9r017 mus musculu P25701 arabidopsis P25702 arabidopsis O92925 rickettsia O41396 spinacia O P06398 coturnix co p42759 arabidopsis O2726 archaeoglob O97730 streptococc P91753 lytechinus Q13568 homo sapina
ZAP3_MOUSE ACP2_ARATH ACP3_ARATH GRPE_KICCN VATE_SPIOL TRT3_COTJA DH10_ARATH DH40_ARATH HEM2_STRPI HEM2_STRPI IRF5_HUMAN UL21_VZVD
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1386 136 136 178 252 252 260 260 283 364 498
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33 3 3 3 3 3 3 3 3 3 4 4 4 4 4 4 5 5 5 5

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
          SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
DATABASE: NAME=Protein Spotlight,
NOTE=ISSUE 16 of November 2001;
WWW="http://www.expasy.org/spotlight/articles/sptlt016.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boundol C., Briggon G., Mahe M.-F., Printz C.; "Characterization of goat allelic alpha s2-caseins A and B: further evidence of the phosphorylation code of caseins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutheleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
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81E7408AF1C12F7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence of the goat alpha s2-casein-encoding cDNA.";
                                                                                                                                                                                                                    Pfam; PF00363; caseins; 2.
PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
Milk; Phosphorylation; Signal; Repeat; Antibiotic.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.3%; Score 103; DB 1;
84.0%; Pred. No. 1.5e-09;
                                                                                                                                                                                                                                                                            ALPHA-S2 CASEIN,
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PHOSPHORYLATION.
PHOSPHORYLATION.
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PHOSPHORYLATION.
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01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCS casein precursor (Alpha-S2-CN).
                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=93216130; PubMed=8462880;
                                                                                                                                                                    EMBL; M16644; AAA30479.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          26019 MW;
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  OR 51-60
                                                                                                                                                                                                PIR; A29087; A29087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9925;
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P33049;
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                                                                                                                                          -!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-!- POLYMORPHISM: THERE ALLIELES OF ALPHA-S2 CASEIN ARE KNOWN: A, B AND
C. THE FREQUENCIES OF THE ALLIELES IS ESTIMATED TO BE 0.85, 0.04
AND 0.11 IN THE FRENCH DAIRY BREEDS 'ALDINE' AND 'SAANEN'.
-!- SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
                                                      Bouniol C., Briggion G., Mahe M.F., Printz C.,
"Biochemical and genetic analysis of variant C of caprine alpha s2-casein (Capra hircus).";
Anim. Genet. 25:173-177(1994).
-i- FUNCTION: IMPORTANT ROLE IN THE CAPACITY OF MILK TO TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ovis aries (Sheep).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W (BY SIMILARITY).
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Pred. No. 3.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26389 MW; 187DEF42FD688291 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pram; PF00363; caseins; 2.
PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
Milk; Phosphorylation; Signal; Repeat; Polymorphism.
STGNAL 1 15 BY SIMILARITY.
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K -> I (IN VARIANT C)
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ALPHA-S2 CASEIN.
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PHOSPHORYLATION
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13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
   Protein Seq. Data Anal. 5:213-218(1993).
                            SEQUENCE FROM N.A. (VARIANT C).
MEDLINE-95030556; PubMed=7943951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 NANEEEYSIRSSSEESAEVAPEEIK 86
                                                                                                                                                                                                                                                                                                                                                                  EMBL; X65160; CAA46278.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001588; Casein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.28;
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                                                                                                                                 CALCIUM PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                              PIR; S20620; S20620.
PIR; JN0547; JN0547.
PIR; S33880; S33880.
PIR; S33881; S33881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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P04654;
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MOD_RES
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Proc. Natl.
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01.FEB-1995 (Rel. 31, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
16-027-2001 (Rel. 40, Last annotation update)
Eye-specific diacylglycerol Kinase (EC 2.7.1.107) (Retinal degeneration A protein) (Diglyceride Kinase 2) (DGK 2) (DAG Kinase 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Canton-S; TISSUE=Head;
MEDLINE=94068563; PubMed=8248222;
MRSDLINE: 1. OKAZAKİ A., Hosoya T., Hotta Y.;
Masai I. OKAZAKİ A., Hosoya T., Hotsophila retinal degeneration A gene encodes an eye-specific incosophila retinal degeneration A gene mocodes and experimental discylglycerol kinase with cysteine-rich zinc-finger motifs and
                                                                           .
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Pred. No. 1.7e-06;
1; Mismatches 6; Indels
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PHOSPHORYLATION (POTENTIAL).
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PHOSPHORYLATION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67212935E27426D7 CRC64;
                                                                                                                                                                                                                         -i- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-i- SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALPHA-S2 CASEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1454 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Intertrain, PP001633; Caseins; 2. PR04 BETA; 1. PR05ITE; PS00306; CASEIN_ALPHA_BETA; 1. Milk; Phosphorylation; Repeat; Signal.
                                                                                                                                                                                                          . - SUBCELLULAR LOCATION: Extracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 NADEEEYSIRSSSEESAEVAPEEVK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26332 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.5%;
72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIK; AZDU/U; KASHSZ.
InterPro; IPR001588; Casein.
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X03238; CAA26983.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223
223
223
23
72
73
74
                  Bovidae; Caprinae; Ovis.
                                                                                                                                                                                           CALCIUM PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ankyrin repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 18; Conserv
                                     NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDGE_DROME
009103;
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VARIANT
SEQUENCE
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                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 90:11157-11161(1993).
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                                                                                                                                                                                                                                                            -i- SIMILARITY: BELONGS TO THE EUKARYOTIC DIACYLGLYCEROL KINASE
                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1454;
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                                             ABSENCE LEADS TO RHABDOMERE DEGENERATION DUE TO DEFECTIVE
                                                                                               -i- CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC-A (POTENTIAL). CATALYTIC-B (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R InterPro; IPRNOUV.DS; DAGNAG.
R InterPro; IPRNO12105; DAG_LE-bind.
R InterPro; IPRNO12105; DAG_LE-bind.
R InterPro; IPRNO13622; DAG_LE-bind.
R FORONTO; DAG_LE-bind; 1.
Pfam; PF000130; DAG_RE-bind; 1.
Pfam; PF000130; DAG_RE; 1.
Probom; P0002039; DAGKa; 1.
R Probom; P0002049; DAGKa; 1.
R Probom; P0002049; DAGKa; 1.
R SMART; SM002049; DAGKa; 1.
R SMART; SM00040; C1; 2.
R SMART; SM00046; DAGKa; 1.
SMART; SM00046; DAGKa; 1.
SMART; SM00046; DAGKa; 1.
R PROSITE; PS50088; ANK_REP_REGION; 1.
R PROSITE; PS50081; DAG_PE_BIND_DOM_1; FALSE_NEG.
R PROSITE; PS50081; DAG_PE_BIND_DOM_2; FALSE_NEG.
R TRANSFERSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G->D: IN MUTANT RDGA2
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                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY - GLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D17315; BAA04135.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0003217; rdgA.
InterPro; IPR002110; ANK.
InterPro; IPR000756; DAGKA.
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                                                                                     PHOSPHOLIPID TURNOVER.
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92 642
52 719
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1346
1379
1415
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                    BINDING DOMAINS
                                                                                                                                                                                                                                                       AFTER ECLOSION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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RESULT 5

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0
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Fibronectin type III domains in yeast detected by a hidden Markov
                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Curr. Biol. 6:1544-1546(1996).
-!- FUNCTION: INVOLVED IN CHITIN SYNTHESIS AND ALSO REQUIRED FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                            Santos B., Duran A., Valdivieso M.H.;
"CHS5, a gene involved in chitin synthesis and mating in
Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.1%; Score 44; DB 1; Length 671;
55.0%; Pred. No. 14;
tive 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson R., Waterston R.; Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                               Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 166 FIBRONECTIN TYPE-III.
671 AA; 73638 MW; FA92741BB62814C2 CRC64;
                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAV-2000 (Rel. 39, Last annotation update)
Chitin biosynthesis protein CHS5 (CAL3 protein).
CHS5 OR CAL3 OR YLR330W OR L8543.18
                          671 AA.
                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae.";
Mol. Cell. Biol. 17:2485-2496(1997).
                        PRT;
                                                                                                                                                                                                                                         MEDLINE=97265380; PubMed=9111317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIBRONECTIN TYPE III DOMAIN.
MEDLINE=97148176; PubMed=8994808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50172; BRCT; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD; S0004322; CHS5.
InterPro; IPR001357; BRCT.
InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z49198; CAA89059.1; -. EMBL; U20618; AAB64526.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 NEEEYSIGXXXEEXAEVATE 22
                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00041; fn3; 1.
Pfam; PF00533; BRCT; 1.
SMART; SM00292; BRCT; 1.
SMART; SM00060; FN3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bateman A., Chothia C
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 11; Conserva
                                                                                                                                                                               NCBI_TaxID=4932;
                 CHS5_YEAST
Q12114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
CHS5_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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278 NEEELSYSKENEPVAEVADE 297

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=S288C / AB972;
MEDLINE-97313267; PubMed-9169871;
Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Widner W.R., Wickner R.B., "Evidence that the SKI antiviral system of Saccharomyces cerevisiae acts by blocking expression of viral mRNA."; Mol. Cell. Biol. 13:4331-4341(1993).
                                                                                                                                                                                                             MEDLINE-8929722; Pubbed-2544911; Priefer U.B., Kalinowski J., Rueger B., Heumann W., Puehler A.; "ISR1, a transposable DNA sequence resident in Rhizobium class IV strains, shows structural characteristics of classical insertion
                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Ekaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 1; Length 88;
Pred. No. 2.5;
1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                         01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Insertion element ISR1 hypothetical 10 kDa protein A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002514; Transposase_8.
Pfam; PF01527; Transposase_8; 1.
Hypothetical protein; Transposable element.
SEQUENCE 88 AA; 10024 MW; 64B7027A9FB7DB10 CRC64;
                                                                                                                                                                                                                                                                                         Plasmid 21:120-128(1989).
                       88 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-F81-1994 (Rel. 28, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CGT-2001 (Rel. 40, Last annotation update)
Antiviral protein SKI2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1287 AA
                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=93309467; PubMed=8321235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X06616; CAA29830.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 EEYSIGXXXEEXAEVATEEV 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 EEQIIGILREQEAGVATAEV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKI2 OR YLR398C OR L8084.17.
                STANDARD;
                                                                                                                                       Rhizobiaceae; Rhizobium.
NCBI_TaxID=391;
                                                                                                                                                                                                   STRAIN-Class IV strains;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
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                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S09659;
              YIA3_RHISP
P17985:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKI2_YEAST
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YIA3_RHISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKI2_YEAST
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Neurofilament triplet L protein (68 kDa neurofilament protein) (Neurofilament light polypeptide) (NF-L) (Micro glutamic acid-rich

orotein).

Bos taurus (Bovine). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;

SECUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antiviral; Translation regulation; RNA-binding; DNA-binding; Helicase;
Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,
Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,
Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kotter P.,
Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Mostl D.,
Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
Underwood A.D., Urrestarazu L.A., Vandenbol M., Verhasselt P.,
Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
"The nucleofide sequence of Saccharomyces cerevisiae chromosome XII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                   Lygerou 2., Conesa C., Lessage P., Swanson R.N., Ruet A., Carlson M., Sentenac A., Seraphin B.;
Sentenac A., Seraphin B.;
Sentenac A., Seraphin B.;
Sentenac B. Brif gene encodes a transcription factor involved in the expression of a broad class of genes including snRNAs.";
Nucleic Acids Res. 22:5332-5340(1994).
-!- PUNCTION: REPRESSES DSRNA VIRUS PROPAGATION BY SPECIFICALLY
BLOCKING TRANSLATION OF VIRAL MNNAS, PERHAPS RECOGNIZING THE ABSENCE OF AN REPLICON. SERWS TO BE A HELICASE.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-! SIMILARITY: BELONGS TO THE HELICASE FAMILY. SKIZ SUBFAMILY.
                                                                                                                                                                                                                                                                                       MINITE = 55116323; PubMed-7816623; Eygerou Z., Conesa C., Lesage P., Swanson R.N., Ruet A., Carlson M., Lyqerou Z., Conesa C., Lesage P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA-BINDING RGG-BOX (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7CCD36CFC0DF8C32 CRC64;
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QM \to L \text{ (IN REF. 1)}.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146058 MW;
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SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L13469; AAA35049.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z18944; CAA79378.1; -.
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Matches 11; Conservative
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                                                                                                                                                                                                                   Nature 387:87-90(1997).
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556 57
555 59
326 32
759 76
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                                                                                                                                                                                                                                                                          STRAIN-S288c;
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SITE
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MEDLINE=85154567; PubMed=3884373; Isobe T., Okuyama T.; "Brain micro glutamic acid-rich protein is the C-terminal endpiece of the neurofilament 68-kba protein as determined by the primary

STRAIN-HOLStein; TISSUE-Brain; Hill W.D., Zhang L., Balin B.J., Sprinkle T.J.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

SEQUENCE OF 468-554

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FEBS Lett. 182:389-392(1985).

-!- FUNCTION: NEUROPILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, H, WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURORAL CALIBER.

-!- DOMAIN: THE EXTRA MASS AND HIGH CHARGE DENSITY THAT DISTINGUISH THE NEUROFILAMENT PROTEINS FROM ALL OTHER INTERMEDIATE FILAMENT PROTEINS FROM ALL OTHER INTERMEDIATE FILAMENT A CHARGED SCAFFOLDING STRUCTURE SUITABLE FOR INTERACTION MITH OTHER NEURONAL COMPONENTS OR IONS.

-!- MISCELLANEOUS: NP-L IS THE MOST ABUNDANT OF THE THREE NEUROFILAMENT PROTEINS AND, AS THE OTHER NONEPTHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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TAIL, SUBDOMAIN B (ACIDIC).
MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D772B81CA2C31C1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEAD (BY SIMILARITY).
ROD (BY SIMILARITY).
TAIL (BY SIMILARITY).
COIL 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Intermediate filament; Coiled coil; Neurone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U83919; AAB41543.1; -.
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Query Match
Best Local Similarity 45.83
Matches 11; Conservative
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509
554 AA;
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125
138
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NFL_BOVIN STANDARD; PRT; 554 AA. P02548; P79127; 21-JUL-1986 (Rel. 01, Created) 21-JUNOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)

DI DI DI

NFL_BOVIN

RESULT 8

246 EEEKSAKSISEEIMEEATEE 265

g

394 L -> V (IN REF. 2). 60948 MW; 17203441C7F6AAB7 CRC64;

562 AA;

CONFLICT

FT

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                                                                                                                                                                                                                                                                                                               Meinhardt F., Busskamp M., Wittchen K.D.;
"Cloning and sequencing of the leu C and npr M genes and a putative spo IV gene from Bacillus megaterium DSM319.";
Appl. Microbiol. Biotechnol. 41:344-331(1994).
                                                                                                                                                                                                  Nuhn S., Fortnagel P.; Molecular cloning and nucleotide sequence of the gene encoding a
                                                                                                                                                                                                                                                                                                                                                   calcium-dependent exoproteinase from Bacillus megaterium ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metalloprotease; Zinc; Calcium; Zymogen; Signal.
1 24 POTENTIAL.
25 245 ACTIVATION PEPTIDE (POTENTIAL).
                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Bacillolysin precursor (EC 3.4.24.28) (Neutral protease).
                                                                                                                          Firmicutes; Bacillales; Bacillaceae; Bacillus,
                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: BINDS 1 ZINC ION AND FOUR CALCIUM IONS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S -> N (IN REF. 2).
A -> G (IN REF. 2).
A -> A (IN REF. 2).
A -> T (IN REF. 2).
R -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Secreted.
                               562 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACILLOLYSIN
                                                                                                                                                                                                                                                   Gen. Microbiol. 139:39-47(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam: PF01447; Peptidase_M4; 1.
Pfam: PF01447; Peptidase_M4; 1.
Pfam: PF03413; Pep_M4_propep; 1.
PRINTS; PR00730; THERMONYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR005075; Pep_M4_propep.
InterPro; IPR001570; Peptidase_M4.
                                                                                                                                                                                   MEDLINE=93195511; PubMed=8450307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                       STRAIN-DSM 319;
MEDLINE-94288995; PubMed-7764969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X75070; CAA52964.1; -.
                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
186
251
302
344
                                                                                                              Bacillus megaterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000130;
                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=ATCC 14581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1NPC.
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                      NCBI_TaxID=1404;
                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                           thermolysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; M04.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P05806;
                         NPRM_BACME
Q00891;
                                                                                                                           Bacteria:
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METAL
METAL
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CONFLICT
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RESULT 9
NPRM_BACME
                                                                                                                                                                                                                                      14581.
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                                                                                                                                                                                                                                                                                                                                                                 Voss H., Benes V., Andrade M.A., Valencia A., Rechmann S., Teodoru C., Schwager C., Paces V., Sander C., Ansorge W.; "DNA sequencing and analysis of 130 kb from yeast chromosome XV."; Yeast 13:655-672(1997).
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Who's who among the Saccharomyces cerevisiae actin-related proteins? A classification and nomenclature proposal for a large family."; Yeast 13:1053-1058(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
Score 42; DB 1; Length 562;
Pred. No. 25;
                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.3%; Score 42; DB 1; Length 881; 36.0%; Pred. No. 39; 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100208 MW; 8174851B6B077A19 CRC64;
                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ACEIN-like protein ARPB.
ARPB OR YOR141C OR YOR334BC.
                                                                                                                                                                881 AA.
                             6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-ASP
                                                                                                                                                             PRT;
                                                    1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                         MEDLINE=97344368; PubMed=9200815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97435478; PubMed=9290209;
Poch O., Winsor B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 NANENELGSSRDKRAPPAVQTSK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NANEEEYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structural protein; Cytoskeleton.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGD; 30005667; ARPB
InterPro; IPR004000; Actin_like.
Pfam; PF00022; actin; 2.
SMART; SM00268; ACTIN; 1.
 39.3%;
32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X94335; CAA64058.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z75049; CAA99341.1; -.
                            Conservative
                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 39.3
Best Local Similarity 36.0
Matches 9; Conservative
              Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                881 AA;
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
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8
                                                                                                                                                        ARP8_YEAST
Q12386;
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENE NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                            ARP8_YEAST
                            Matches
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                                                                                                                            RESULT 10
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YB4F_SCHPO
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-I- FOUNTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.

-I- DOMAIN: THE EXTRA MASS AND HIGH CHARGE DENETRY THAT DISTINGUISH THE NEUROFILAMENT PROTEINS FROM ALL OTHER INTERMEDIATE FILAMENT PROTEINS FROM ALL OTHER INTERMEDIATE FILAMENT A CHARGED SCAFFOLDING STRUCTURE SUITABLE FOR INTERACTION WITH OTHER NEURONAL COMPONENTS OF IONS.

-I- MISCELLANGOUS: NP-L IS THE MOST ABUNDANT OF THE THREE NEUROFILAMENT PROTEINS AND, AS THE OTHER NONEPITHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                          Geisler N. Kaufmann E., Fischer S., Plessmann U., Weber K.;
Geisler N. Kaufmann E., Fischer S., Plessmann U., Weber K.;
Neurofilament architecture combines structural principles of
intermediate filaments with carboxy-terminal extensions increasing
in size between triplet proteins.";
EMBO J. 2:1295-1302(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAIL, SUBDOMAIN B (ACIDIC).
O-LINKED (GLCNAC) (BY SIMILARITY).
O-LINKED (GLCNAC) (BY SIMILARITY).
EPITOPE (RECCONIZED BY IF-SPECIFIC MONOCLONAL ANTIBODY).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
putative ATP-dependent RNA helicase ZK686.2 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  !- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 1; Length 548; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Intermediate filament; Coiled coil; Neurone; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 13; Indels
                                                                                                                             Geisler N., Plessmann U., Weber K.; "The complete amino acid sequence of the major mammalian neurofilament protein (NF-L)."; FEBS Lett. 182:475-478(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83044813637AC739 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAIL, SUBDOMAIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  696 AA
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LINKER 2.
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                                                                                                               MEDLINE=85154583; PubMed=3920075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61940 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.8%;
                                                                                                                                                                                                                                                   SEQUENCE OF 1-82 AND 278-548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00038; filament; 1. PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001664; IF.
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270
279
395
442
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es 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     548 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A02963; OFPGL
                                                     NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTI.AMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YO12_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P34668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZK686.2
                                                                                                      SECUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YO12_CAEEL
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                  δλ
                                                                                                                                                                                                                                                                                           RA MEDLINE=21848401; FUDDMed=11859360;

RA MOOd V., Gwilliam K., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Squuros J., Peat N., Hayles J., Chillingworth T., Churcher C.M.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gonlies M., Gonlor R., Hawlin N., Harris D., Hidalgo J., Hodgson G.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Moule S., Sunders M., Sagueres R., Sharp S.,

RA RA Skelton J., Simmonds M., Squares R., Staren T., Whitehead S.,

RA RA Skelton J., Simmonds M., Squares R., Staren T., Whitehead S.,

RA RA RA Stares R., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Gabel C., Fuchs M., Fritzc C., Lehrach H., Reinhardt R., Pohl T.M.,

RA Gabel C., Fuchs M., Fritzc C., Lehrach H., Reinhardt R., Pohl T.M.,

RA Gabel C., Fuchs M., Gaillardin C., Moore K., Hurst S.M.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Calibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Calibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shakovski G.V., Ussery D., Barrell B.G., Nurse P.,

RA Nature 415:871-880(2002).

C. Stilzcsaccharomyces pombe.";

RE INTER RE INTERIATION PREST YNL124W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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16-0cT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet L protein (68 kDa neurofilament protein)
(Neurofilament light polypeptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.8%; Score 41.5; DB 1; Length 516; 36.0%; Pred. No. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 516 AA; 57639 MW; 22597CE8E5AF9B5F CRC64;
                                                                                                                                      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                           15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C30D10.15 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Mismatches
                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 NPSEQEFS----DDEAEVAAKQLK 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
01-0CT-1996 (Rel. 34, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z97992; CAB10810.1; -.
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les 9; Conserva
                                                                                                                                                                                            Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
                                                                                                                                                                                                              NCBI_TaxID=4896;
                                                                                                      SPBC30D10,15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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P02547;
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Gaps

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Matches
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                                                                                                                                                          Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Latreille P., Lighthing J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Ropera A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Walston J., Thierry Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterian R., Watson A., Weinstock L., Wilkinson-Sproat J., K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.3%; Score 41; DB 1; Length 696; 40.0%; Pred. No. 45; ive 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; Froc.
Pfam; PF00271; hellow,
Pfam; PF00271; hellow,
SMART; SW00487; DEXDC; 1.
PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
Hypothetical protein; Helicase; ATP-binding; RNA-binding.
ATP (BY SIMILARITY).
377 ATP (BY SIMILARITY).
377 ATP (BY SIMILARITY).
377 ATP (BY SIMILARITY).
CGEGEF997FAA7FA2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elegans.,

Auture 368:32-38(1994).

-! FUNCTION: PROBABLE ATP-BINDING RNA HELICASE.

-!- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Camelus dromedarius (Dromedary) (Arabian camel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAS2_CAMDR STANDARD; PRT; 193 AA. 097944; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=Somali, TISSUE=Udder;
MEDLINE=98291310; PubMed=9627840;
                                                                             SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 NGNEDDESVGNDVAEPME--TEDVE 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S44912; S44912.

WormPep; ZK686.2; CE00456.

InterPro; IPR001410; DEAD.

InterPro; IPR000629; DEAD.

InterPro; IPR001650; Hellcase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00270; DEAD; 1.
Pfam; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L17337; AAA28223.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 40.09 tes 10; Conservative
                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9838;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CY. Columbia;
STRAIN-CY. Columbia;
MEDLINE-21016720; PubMed-11130713;
Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
Wincker P., Cattolico L., Weissenbach J., Saurin M., Quetier P.,
Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thalland (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89160348; PubMed-2922299;
Post-Beittenmiller M.A., Hlousek-Radojcic A., Ohlrogge J.B.;
"DNA sequence of a genomic clone encoding an Arabidopsis acyl carrier
Kappeler S., Farah Z., Puhan Z.;
"Sequence analysis of Camelus dromedarius milk caseins.";
J. Dairy Res. 65:209-222(1998).
-!- FUNCTION: IMPORTANT ROLE IN THE CAPACITY OF MILK TO TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN 16 193 ALPHA-S2 CASEIN.
SEQUENCE 193 AA; 22964 MW; 2843256F8FDZED13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-Beittenmiller M.A.;
Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases
                                                                                                            -!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: MAMMARY GLAND; MILK
-!- SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acyl carrier protein 1, chloroplast precursor (ACP).
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; LERVOLDOUGH, 2.
Pram: PP00363; cascins; 2.
PROSITE; PS00306; CASEIN_ALPHA_BETA; FALSE_NEG.
Milk; Phosphorylation; Signal.
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.9%; Score 40.5; I
52.4%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 17:1777-1777(1989)
                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ012629; CAA10078.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 NTEQLSI---SEESTEVPTEE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 NEEEYSIGXXXEEXAEVATEE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 52.49 tes 11; Conservative
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                                                                                         CALCIUM PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Columbia;
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P11829;
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RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Corrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J. Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Gooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Roney T., Rizzo M., Walts A., Utterback T., Fulia C.Y., Shea T.P.,
RA Roney T., Rizzo M., Walts A., Utterback T., Fulia C.Y., Shea T.P.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Walte O., Venter J.C.,
RA Fraser C.M., Matsumoto M., Matsuno A., Muraki A.,
RA Sasamoto S., Kimura T., Idessawa K., Kawashima K., Kishida Y.,
RA Watanabe A., Yamada M., Tabata S.,
RA Watanabe A., Yamada M., Tabata S.,
RA Watanabe A., Yamada M., Tabata S.,
RA Haliana.,
RA Haliana.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Physiol. 98:206-214(1992).

-!- FUNCTION: ACYL CARRIER PROTEIN IS A KEY COMPONENT IN DE NOVO FATTY

-!- FUNCTION: ACYL CARRIER PROTEIN IS A SWALL ACIDIC PROTEIN WITH A 4'-PHOSPHO-
ACID BIOSYNTHESIS. IT IS A SWALL ACIDIC PROTEIN WITH A 4'-PHOSPHO-
PANTETHEINE PROSTHETIC GROUP, ATTACHED THROUGH A SERINE, TO WHICH
GROWING FATTY ACID CHARIS ARE COVALENTLY BOUND.

-!- SIMILARITY: CONTAINS 1 ACYL CARRIER DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hlousek-Radojcic A., Post-Beittenmiller D., Ohlrogge J.B.; "Expression of constitutive and tissue-specific acyl carrier protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACYL CARRIER PROTEIN 1.
PHOSPHOPANTETHEINE (BY SIMILARITY).
6AA3431A78640CGD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.4%; Score 40; DB 1; Length 137; 40.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PP00550; pp-binding: 1.
ProDom; PD000887; Acyl_carrier; 1.
ProBom; PS0012; PCV1_carrier; 1.
PROSITE: PS0012; PHOSPHOPANTETHEINE; 1.
PROSITE; PS0075; ACP_DOMAIN: 1.
Fatty acid blosynthesis; Phosphopantetheine; Chloroplast; Transit peptide; Multigene family.
TRANSIT 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003231; Acyl_carrier.
InterPro; IPR003880; Ppantne_attach.
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EMBL; AC009465; AAG51406.1; -.
PIR; S03267; S03267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isoforms in Arabidopsis.";
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Best Local Similarity
Matches 8; Conserv
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4 EEBYSIGXXXEXAED 23

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104 EEEFNIOMAEEKAOKIATVE 123

Search completed: February 11, 2003, 18:17:46 Job time : 12.0825 secs

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(without alignments)
183.363 Million cell updates/sec
                                                                                     February 11, 2003, 18:13:41; Search time 28.0928 Seconds
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                              671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
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sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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sp_rodent:*
sp_virus:*
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1: sp_archea:*
2: sp_bacteria:*
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Maximum DB seq length: 200000000
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107
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10:
11:
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	O62825 bubalus bub	. Q9myu7 capra hircu	capra	O9myu6 capra hircu	Q99k07 capra hircu	Q8wr09 drosophila	Q8stb9 drosophila	Q8wr08 drosophila	Q9v7i7 drosophila	Q8stl0 encephalito	Q9srd2 arabidopsis	Q9w3a4 drosophila	drosc	Q9up59 homo sapien	homo	Q12820 homo sapien
ID	062825	O9MYU7	09TT07	90XM60	Q9GK07	O8WR09	08STB9	Q8WR08	717760	Q8STL0	Q9SRD2	Q9W3A4	08SY47	09UP59	095228	012820
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% Query Match Length DB	210	124	223	223	223	914	465	1179	1277	414	1280	1417	1457	526	528	562
% Query Match	96 3	82.2	82.2	82.2	82.2	46.7	46.7	46.7	46.7	44.9	43.9	43.5	43.5	43.0	43.0	43.0
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	o o o o o o o o o o a a a
11117 1117 1222 1222 1333 1333 1333 1334 1335 1335 1335 1335	3 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

																0;				
210 AA.	Created) Last sequence update)	17, Last annotation update)	Bubalus bubalis (Domestic water buffalo). Bubarus batazoa: Chordata: Craniata; Vertebrata; Buteleostomi;	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;				was properties and a company in B.	"Cloning and nucleotide sequence of convencing as cases. In the convencion of the co	nk/DDBJ databases.				0.000 0.000	303F1134C CNC047	8 6; Length 210; 8-10; 4; Indels 0; Gaps				124 AA.
	d) equen	nnota	ffalc iata;	a; Ru				4	T CDI	enBar				3000	JEFYO	NO.				
PRT;	Created) Last seq	ast a	er bu	lactyl				0	suce o	SMBL/G						Score 103; D) Pred. No. 6.90 0; Mismatches		VK 73		PRT;
PRELIMINARY;	(TrEMBLrel.	(TrEMBLrel. Fragment).	Bubalus bubalis (Domestic water buffalo).	; Eutheria; Cetartiod	Bovidae; Bovinae; Bubalus. NCBI_TaxID=89462;	[1]	TISSUE=MAMMARY GLAND;	Das P., Jain S., Garg L.C.;	and nucleotide seque	bubalis."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases	EMBL; AJ005431; CAA06534.2; -	InterPro; IPR001588; Casein.	Pfam; PF00363; caseins; 2.		210 AA; 24/00 MW;	96.3%; Similarity 84.0%; 1; Conservative	NANEEEYSIGXXXEEXAEVATEEVK	NANEEEYSIGSSSEESAEVATEEVK		PRELIMINARY;
LT 1 25 062825	O62825; 01-AUG-1998 01-NOV-1999	01-JUN-2001 AS2-casein (Bubalus B	Mammalia	Bovidae; NCBI_Tax	[1]	TISSUE=M	Das P.,	"Cloning	bubalis.";	EMBL; AJ	InterPro	Pfam; PF	NON_TER	SEQUENCE	Query Match Best Local Matches 2	1 NAN	49 NAN	RESULT 2	ZOVMEQ
RESULT 062825 ID 06	AC DT	DE	SO	88	88	RN	R S	RA	RT	RT	DR	DR	DR	FT	ÖS	QAX	Qy	qq	RES	Q9MYU7 ID Q

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                                                                          Capra hircus (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Capra hircus (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
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                                                                                                                                                              EBOUENCE FROM N.A.
Lagonigro R., Pilla F., Matassino D., Zullo A.;
Lagonigro R., Pilla F., Matassino D., Zullo A.;
"Sequence of goat alpha s2-casein allele 0 encoding cDNA.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL289715, CAB94235 1. -
InterPro; IPR001588; Casein.
PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
SEQUENCE 124 AA; 14533 MW; C363E536CC17B5F2 CRC64;
                                                                                                                                                                                                                                                                                                             Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.2%; Score 88; DB 6; Length 223; 72.0%; Pred. No. 3e-07;
                                                                                                                                                                                                                                                                                         82.2%; Score 88; DB 6; Length 124
72.0%; Pred. No. 1.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEQUENCE FROM N.A.

Veltri C.C., Pilla F.F., Lagonigro R.R.;
"A new allele of goat alpha s2-casein.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ249995; CAB59920.1;
InterPro; IPR001588; Casein.
Fram; PF00363; caseins; 2.
PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
SEQUENCE 223 AA; 26433 MW, CE9F4DCBD768R293 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CASEIN_ALPHA_BETA; 1.
; 26433 MW; CE9F4DC8D7688293 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                1 NANEEFYSIGXXXEEXAEVATEEVK 25
                                                                                                                                                                                                                                                                                                                                                                                 62 NANEEEYSIRSSSEESAEVAPEEIK 86
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                                                                                                                      Bovidae; Caprinae; Capra.
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Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capra hircus (Goat).
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                                               Alpha s2-casein.
CSN1S2.
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CSN1S2.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Capra hircus (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.2%; Score 88; DB 6; Length 223; 72.0%; Pred. No. 3e-07; tive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.2%; Score 88; DB 6; Length 223; 72.0%; Pred. No. 3e-07;
                                                                                                                                                                     Lagonigro R., Pilla F., Matassino D., Zullo A.;
Lagonigro R., Pilla F., Matassino D., Zullo A.;
A new allele of goat alpha s2-casein gene.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJZ89716. CAB94236.1;
InterPro; IPR001588; Casein.
PROSITE; PS00363; caseins; 2.
PROSITE; PS00366; CASEIN.AI.PHA_BBTA; 1.
SEQUENCE 223 AA; 26403 MW; OEIFEB3F24DA8552 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Veltri C., Pilla F., Lagonigro R.;
A new allele of alpha S2-casein.";
Submitted (AAn-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ297310; CAC21704.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        914 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ297311; CAC21704.2; JOINED. EMBL; AJ242728; CAC21704.2; JOINED. EMBL; AJ297312; CAC21704.2; JOINED. EMBL; AJ297313; CAC21704.2; JOINED. EMBL; AJ297314; CAC21704.2; JOINED. EMBL; AJ297315; CAC21704.2; JOINED. EMBL; AJ297315; CAC21704.2; JOINED. EMBL; AJ297315; CAC21704.2; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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EMBL; AJ242526; CAC21704.2; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 NANEEEYSIRSSSEESAEVAPEEIK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ242528; CAC21704.2; JOINED EMBL; AJ242533; CAC21704.2; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 NANEEEYSIGXXXEEXAEVATEEVK 25
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 72.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha s2-casein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9925;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Q9GK07
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Q8WR09
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Query Match
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Moscomorpha; Ephydroidea; Drosophilldae; Drosophilldae; Drosophilldae; Drosophilldae; Drosophilldae; Drosophila; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapheton M., Brokstein P., Hong L., Agbayani A., Carlson J., Stapheton M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S., Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

FMBL, Ar61011 AAL65369.1; -

EMBL, A7069076; AAL39221.1; -

ERBL, A7069076; AAL39221.1; -
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                          STEATM-CANTON S;
Takeuchi K.-I., Yamaguchi A., Kaneda M., Aizu M., Umeda M.;
Takeuchi K.-II., Yamaguchi A., Kaneda M., Alzu M., Umeda M.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF461099; AAL66367.1; -.
SEQUENCE 914 AA; 102660 WW; E255B90EA9DDA76C CRC64;
                                                                                                                                                                                                                                                                                                                                                        Score 50; DB 5; Length 914; Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
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01-MAR-2002 (TrEMBLrel. 20, Created)
11-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Dystroglycan type II (GH09323p).
      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              997 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -JUN-2002 (TrEMBLrel. 21, Created)
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                                                                                                                                                                                                                                                                                                                                                                   46.78;
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                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                           Dystroglycan type III.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Adams N. D., Celniker S. E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu D.A., Burlen B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller C., Davenport L.B., Dayles P.,
RA Glork M., Doyle C., Correr A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller R., Mays A.D., Dew I., Dietz S.M.,
RA Ballew R.M., Boulen A.E., Downes M., Dugan-Rocha S., Plaischmann W.,
RA Clork M., Gorrell J.H., Guz., Gune P., Harris M.,
RA Dockon K., Gorrell J.H., Guz., Gune P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., March M., Classer K.,
RA Jalali M., Rallush F., Karpen G.H., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y. Levitsky A.A., IJ J., Li Z., Liang Y., Lin X.,
Ander D., Milshian N.V., Mobarry C., Morris J., Mosherson D.,
RA Mount S.M., Now M., Murphy B., Murphy E., Wassarman D.A., Stung A., Nang X.,
RA Reinerf K., Remington K.A., Nixon K., Murskern D.R., Palacher F., Shen H.,
RA Reinerf K., Remington M., Stungson M., Stung A., Hang X., Yoo Q.A.,
RA Syliskas R., Teetor C., Turner R., Venter E., Wang X., Yao Q.A.,
RA Wilshas R., Teetor C., Turner R., Venter E., Wang X., Yao Q.A.,
RA Wang Z.-Y., Woodage T., Worler E., Woodage T., Woolage D., Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Dystroglycan type I.

Drosophila melanogaster (Fruit fly).

Brkaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Metazoa; Arthropoda; Tracheata; Brachycera; Muscomorpha;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                                                                                                                                                                                                                                                      Takeuchi K.-I., Yamaguchi A., Kaneda M., Aizu M., Umeda P. Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF461100; AAL66368.1; - SEQUENCE 1179 AA, 129583 MW; 46B07681A606BBEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1277 AA.
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ANEEEYSIGXXXEEXAEVATE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.78;
47.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 47.6
Matches 10; Conservative
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DG OR CG18250.
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Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000) .

EMBL; Ab003808; AAF58068.1; -
Flybase; FBgn0034072; Dg.

SEQUENCE 1277 AA; 139496 MW; C54961844ABB067A CRC64;
                                                                                                                                                                                          Gaps
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Dernsier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Welssenbach J., Vivares C.P., Saurin W., Gouy M., Gonome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
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                                                                                                                                                 Score 50; DB 5; Length 1277; Pred. No. 8.7;
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                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Encephalitozoon cuniculi.
Eukaryota, Microsporidia, Unikaryonidae, Encephalitozoon.
NCBI_TaxID=6035,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Putative translation initiation factor IF-2, 73082-68138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 414:450-453(2001).
EMBL; AL590451; CAD27161.1; -.
Hypothetical protein.
SEQUENCE 414 AA; 47375 MW; 0C96540DEC2D9EDA CRC64;
                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical protein ECU09_1880.
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01-MAY-2000 (TrEMBLrel. 13, Last second
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                                                                                                                                                              47.68;
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nes 10; Conservative
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RY STANDALE ERRELEY.

RX Adams N. A.

RADLINE=20196006; PubMed=10731132;

RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D. Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Adams M.D. Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M. Henderson S.N.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Ffeiffer B.D.,

RA Abril J.F., Apdbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botther P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botther P.,

RA Borkova D., Botchan M.R., Doug L.E., Dallike C., Davenport L.B., Davies P.,

RA Geralos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Durbin K.J., Evangelista C.C., Ferriaz S., Fleischmann W.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston R.A., Howland T.J., Well M., Classer K.,

RA Hostin D., Houston R.A., Howland T.J., Well M., Lai Z.,

RA Hostin D., Houston R.A., Howland T.J., Well M. Housh D., Lai Z.,

RA Hostin D., Houston R.A., Howland T.J., Well M. C., Lai Z.,

RA Hostin D., Routs R. C.C., Kratitz S., Kulp D., Lin X.,

RA Hostin D., Mouston R.A., Howland T.J., Well M. H., Libegwan C.,

RA Hostin D., Houston R.A., Howland T.J., Well M. Howlerson D.,

RA Hostin D., Mouston R.A., Montosh M., Nobshrefi A.,

RA Hostin D., Mouston R.A., Mixon K., Nusskern D.R., Pacleb D.M.,

RA Neulov G., Milshina N.V., Mobarty C., Morris J., Publes D.M.,

RA Neulov G., Milshina N.V., Mobarty C., Morris J., Publes D.M.,

RA Nelson D.R., Nelson D.R., Pollard J., Pullson D.M.,

RA Nelson D.R., Nelson R.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Paleson W.A., Pollard J., Pullson D.M.,

RA Nelson D.R., Paleson W.B., Pollard J., Pullson D.M.,

RA Nelson D.R., Paleson W.B., Pollard J., Pullson D.M.,

RA Nelson D.R., Paleson W.B., Pollard J., Pullson D.M.,

RA Nelson D.R., Pale
                                         STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
Maiti R., Ronning C.M., Koo H., Fujli C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Arabidopsis thaliana chromosome 1 BAC F28016 genomic sequence.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC010718; ARA024442.1.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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TIGREAMS; TIGR00231; small_GTP; 1.
GTP-binding; Initiation factor; Protein biosynthesis.
SEQUENCE 1280 AA: 140708 MW; BCIAZBF758859D0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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6; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Last second
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Interpro; IPR00795; EF_CTPbind.
Interpro; IPR005225; Small_CTP.
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PF03144; GTP_EFTU_D2; 1.
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es 9; Conserv
                      SEQUENCE FROM N.A.
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RDGA OR CG10966.
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RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Sturong R., Sun E.,
A Sylirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Sylirskas R., Wassarman D.A., Welnstock G.M., Welssenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Genome sequence of Incorp. Shou X., Zhu X., Smith H.O.,
RA Scibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT Science 287:2185-2195(2000).
RE Science 287:2185-2195(2000).
RE Science 287:2185-2195(2000).
RE FlyBase; FBgn0003217; rdgA.
RICHEPPO: IPR001206; DAGKa.
RICHEPPO: IPR001206; DAGKa.
RICHEPPO: IPR001209; DAG_Kin_cat.
RICHEPPO: IPR001219; DAG_EPE-bind.
R Pfam; PF00003; ank; 4.
R Pfam; PF00003; ank; 4.
R Pfam; PF00009; DAG_RS: 1.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.5%; Score 46.5; DB 5; Length 1417; 50.0%; Pred. No. 40; tive 1; Mismatches 9; Indels 3;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GH23785p.
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PROSITE; PS50297; ANK_REP_REGION; 1.
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ProDom; PD002939; DAGKa; 1.
ProDom; PD005043; DAG_kin_cat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00109; C1; 2.
SMART; SM00045; DAGKa; 1.
SMART; SM00046; DAGKC; 1.
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Matches 13; Conservative
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NCBI_TaxID=7227;
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MEDLINE-9842414; PubMed-9750192; Gruber I., Gruber I., Guurajan R., Lahti J.M., Grenet J., Easton J., Gruber I., Ambros P.F., Kidd V.J.; Publication of a genomic region containing the Cdc2L1-2 and MMP21-22 genes on human chromosome 1p36.3 and their linkage to D122."; Genome Res. 8:929-939(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98424414; PubMed-9750192; MEDLINE-98424414; PubMed-9750192; MEDLINE-98424414; PubMed-9750192; MEDLINE-98424414; Dahti J.M., Grenet J., Easton J., Gruber I., Gururajan R., Lahti J.M., Grenet J., Easton J., Gruber I., Ambros P.F., Kidd V.J.; Puplication of a genomic region containing the Cdc2L1-2 and MMP21-22 genes on human chromosome 1936.3 and their linkage to DIZ2."; Genome Res. 8:929-939(1998.1)
--- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
--- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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SEQUENCE 526 AA; 59272 MW; 3DFF4854ED82B81B CRC64;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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EMBL; AF007525; AAC72090.1; -.
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.0%; Score 46; DB 4; Length 526; 47.6%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
PITSIRE protein kinase beta SV13 isoform.
                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
PITSLRE protein kinase alpha SV4 isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             528 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                    526 AA
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Probom; PD00001; Euk_pkinase; 1.
SMART; SM00220; S_TKc; 1.
PROSITE; PS50011; PROFEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P24941; 1B38.
Interpro; IPR000719; Euk_pkinase.
Interpro; IPR002290; Ser_thr_pkinase.
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225 NAEEEEEGSAAIEDAEETTEAATEE 250
                                                                                                                                                                       PRT;
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                    RESULT 14
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Gaps

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13; Conservative

Matches

Best Local Similarity

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 11, 2003, 18:06:55 ; Search time 30.5258 Seconds Run on:

(without alignments) 91.669 Million cell updates/sec

US-09-380-738A-4

1 KNTMEHVXXXEESIIXQETYK 21 Perfect score: Sednence:

BLOSUM62 Scoring table:

908470 seqs, 133250620 residues Gapop 10.0 , Gapext 0.5 Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:* :01

// SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
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// SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
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// SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Casein phosphopept	Sequence of casein	Bos alpha-s2-casei	Anti-acid peptide.	Bovine alpha-S2 ca	Bovine alpha-S2 ca	Anticariogenic pho	Phosphopeptide 3.	Phosphopeptide #3	Anticariogenic pho
2011111100		Ω	AAR32934	AAR47821	AAW66602	AAR42890	AAW32220	AAE17468	AAR28432	AAP71322	AAR14449	AAR28431
		DB	14	15	19	14	18	23	13	ω	12	13
		Query Match Length DB ID	21	21	21	24	222	222	21	20	20	20
	dР	Query Match	95.6	95.6	92.6	92.6	92.6	92.6	92.3	90.1	90.1	90.1
		Score	87	87	87	87	87	87	84	82	82	82
		Result No.		2	3	4	5	9	7	ω	6	10

20 14 AAR32933 20 14 AAR32310 20 15 AAR31239 20 16 AAR6938 22 2 2 AAB17474 223 23 AAE17473 223 23 AAE17474 223 23 AAE17470 223 23 AAE17470 223 23 AAE17470 223 23 AAE17470 224 22 AAE17470 225 20 AAV32705 225 20 AAV32705 226 17 AAW04271 22 2 AAE17475 225 20 AAV32705 226 21 AAB18254 312 22 AAB18254 312 22 AAB18254 312 22 AAB18254 314 22 AAE11080 436 22 AAE1080 436 22 AAE1083 477 22 AAE1083 56 16 AAW13733 742 22 ABEG0981 875 22 ABEG0981	Casein phosphopept Phosphopeptide der	Phosphopeptide 3.	Sequence of casein	Sodium caseinate t	Phosphopeptide T3.	Pig alpha-S2 casei	alpha-S2 c	a-S2 casei	lpha-S2	hircus	Novel human diagno	B.t. neutral prote	Alpha-S2 casein pr	Chlamydia pneumoni	Plasmodium falcipa	Human nervous syst	Drosophila melanog	Human serine-threo	Human serine-threo	Human NIM1 kinase	protein	. protei				Arabidopsis thalia	Human papillomavir	Drosophila melanog	Protease NprL. La	⊂ .		ohila m	human di	Novel human diagno	
	AAR3293	AAR3123	AAR4782	AAR6893	AAB1280	AAE1747	AAE1747	AAE1746	AAE1747	AAE1747	ABG1712	AAW0427	AAE1747	AAY3570	AAB1825	ABB1478	ABB5864	AAE14	AAE14	AAE1108	AAU0351	AAB6562	AAW0551	AAG9839	AAG0901	AAG4389	AAB9844	ABB6193	AAW1373	ABG2098	ABB5991	ABB6192		ABG003	
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22 2 2 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	11	13	14	5	1 1	17	- 6	6	20	2 2	22	23	24	25	26	27	30	000	0.6	31	3.5	i m	34	. v.	36	37	38	36	40	41	4.2	43	44	4.5	•

ALIGNMENTS

AAR32934 standard; Protein; 21 AA. 02-JUL-1993 (first entry) Casein phosphopeptide #8. AAR32934; RESULT 1 AAR32934

Casein; phosphopetide; dental calculus; salts; alkaline metal; alkaline earth metal; Zn/phosphopeptide complex; aggregate; anti-caries; anti-gingivitis.

Synthetic

/label= Phophoserine /label= Phophoserine label= Phophoserine label= Phophoserine Location/Qualifiers Modified-site Modified-site Modified-site Modified-site

92WO-AU00441. 21-AUG-1992; 04-MAR-1993

WO9303707-A.

91US-0748344.

22-AUG-1991;

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                                                                                                                                                                               The sequences given in AAR32927-35 are casein phosphopeptides which can be used to inhibit dental calculus. These peptides are pref. in the
                                                                                                                                                                                           be used to inhibit dental calculus. These peptides are pref. in the form of salts selected from alkaline metal, alkaline earth metal salts such as Na, Ca, Zn, Cu, Al, K, Sr, Mg and Ni salts. These peptides are pref. present as a Zn/Phosphopeptide complex or aggregate. These peptides have anti-calculus potential, and are anti-caries and anti-
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Casein phosphopeptide; dentinal hypersensitivity; therapy; tooth.
                                                                                                  Controlling dental calculus by treating teeth with oral compsns. which contains phospho-peptide(s) having 5-40 amino-acyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ser(P) = post-translationally phosphorylated serine. A mixture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            component
                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treatment of dentinal hypersensitivity - using casein, compon of casein, phospho-protein or phospho-peptide or their salts
                                                                                                                                                                                                                                                                                                                 Length 21;
                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "see also residues 9,10,16"
                                                                                                                                                                                                                                                                                                           95.6%; Score 87; DB 14;
81.0%; Pred. No. 3.7e-09;
ive 0; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of casein phosphopeptide (CPP).
                        (VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYME ) UNIV MELBOURNE. (VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 17; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR47821 standard; peptide; 21 AA.
                                                                                                                                                     Claim 3; Page 20; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                              1 KNTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Ser(P)
                                                                                                                                                                                                                                                                                                                                                                          1 KNTMEHVSSSEESIISQETYK 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92AU-0003221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                    17; Conservative
          (UYME ) UNIV MELBOURNE.
                                                                          WPI; 1993-093685/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-025888/03
                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                          ginglvitis agents.
                                                                                                                                                                                                                                                                                  21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                   Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9400146-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reynolds EC;
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                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                           residues
                                                                                                                                                                                                                                                                                                            Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR47821
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casein; calcium phosphate complex; amorphous calcium phosphate; ACP; phosphopeptide; delivery vehicle; calcium fluoride; calcium deficiency; osteoporosis; osteomalacia; tooth; bone disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a stable calcium phosphate complex including phosphopeptide stabilised amorphous calcium phosphate (ACP) or its derivative, where the phosphopeptide includes the amino acid sequence: Ser(P)-Ser(P)-GLU-GLU. The amorphous phases stabilised by the phosphopeptides are a delivery vehicle for co-localisation of Ca, P and phosphate at the tooth surface in a slow-release amorphous form producing superior anticaries efficacy over prior art. The amorphous phases stabilised by the phosphopeptides are also useful as dietary
                                                                                                                                          Gaps
casein phosphopetides (CPP) and/or their salts may be used in a method for treating dentinal hypersensitivity. Pref. those CPPs contg. the sequence -Ser(P)-Ser(P)-Ser(P)- predominate. The CPPs can be extracted from a casein digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stable calcium phosphate complex including phospho:peptide stabilised amorphous calcium phosphate - useful for treatment of dental caries, calcium malabsorption and bone diseases such as osteoporosis and osteomalacia.
                                                                                                                                        ö
                                                                                                            Length 21;
                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                            Bos alpha-s2-casein X-4P (fl-21) phosphopeptide.
                                                                                                         Score 87; DB 15;
Pred. No. 3.7e-09;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (VICT-) VICTORIAN DAIRY IND AUTHORITY.
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                                                                                                                                                                                                                                                                       AAW66602 standard; peptide; 21 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Ser(P)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "Ser(P)"
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                                                                                                                                                                                  1 KNTMEHVSSSEESIISQETYK 21
                                                                                                                                                                 1 KNTMEHVXXXEESIIXQETYK 21
                                                                                                         95.6%;
81.0%;
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                                                                                                  Query Match
Best Local Similarity 81.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                          21 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                27-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                            Sequence
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AAW32220
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supplements to increase calcium bioavailability and to help prevent diseases associated with calcium deficiencies. They are particularly useful for treatment or prevention of dental caries, calcium malabsorption and bone diseases such as osteoporosis and osteomalacia. The compositions are useful in humans and in veterinary medicine in domestic animals such as cattle, sheep, horses and companion animals e.g. eats and dogs as well as zoo animals. The present sequence represents a phosphopeptide component of a specifically claimed complex.
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The peptide can be used as an anti-acid / anti-ulcer drug. It can also be used in food or drink production and has no side effects. The peptide is prepared from milk whey, or from whey protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New aminoacid peptide(s) with no side-effects - useful as antacid drugs and antiulcer drugs and used in foods and drinks
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 95.6%; Score 87; DB 14; Length 24; Best Local Similarity 81.0%; Pred. No. 4.3e-09; Matches 17; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                    anti-acid; antiulcer; food; drink; side-effect; whey milk;
whey protein condensate; WPC; skimmed milk.
                                                                                                                              95.6%; Score 87; DB 19; Length 21; 81.0%; Pred. No. 3.7e-09; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "residue is phosporylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "residue is phosporylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "residue is phosporylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                AAR42890 standard; peptide; 24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 2; 7pp; Japanese.
                                                                                                                                                                                 1 KNTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                      1 KNTMEHVSSSEESIISOETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92JP-0092163
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                                                                                                                                                                                                                                                                                                               16-MAY-1994 (first entry)
                                                                                                                                               Local Similarity 81.0 nes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 AA;
                                                                                                                                                                                                                                                                                                                                      Anti-acid peptide
                                                                                                               21 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP05262793-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           condensate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                         AAR42890;
                                                                                                                                    Query Match
                                                                                                                                                             Matches
                                                                                                                                                                                                                                             RESULT 4
                                                                                                                                                                                                                                                      AAR42890
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                                                                                                                                                                                     δλ
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Bovine; alpha-52 casein; dermatological; antiinflammatory; fibroblast; collagen; kerathocyte; skin regeneration; medicament; toothpaste; aging; chewing gum; cosmetic; wrinkling; periodontal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents bovine alpha-52 casein precursor. Peptides having an amino acid sequence which is substantially identical to the C-terminal end of an alpha-52 casein precursor, are used for manufacture of a medicament or foodstuff for promoting growth in humans or animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Manufacture of medicament or foodstuff for promoting growth - using peptide(s) with a sequence identical to the C-terminal end of an alpha-S2 casein precursor
                                                                                                                                                                                                                                                                                          Bovine alpha-S2 casein precursor; growth promoting; mitogenic assay; platelet-derived growth factor; insulin-like derived growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.6%; Score 87; DB 18; Length 22.81.0%; Pred. No. 4.8e-08; Pred. No. 4.8e-08; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine alpha-S2 casein precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE17468 standard; Protein; 222 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 3; 33pp; English.
                                                                                                                                       AAW32220 standard; protein; 222 AA
                                                                                                                                                                                                                                                              Bovine alpha-S2 casein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu Q, Smith JA, Wilkinson MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 KNTMEHVSSSEESIISQETYK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KNTMEHVXXXEESIIXQETYK 21
1 KNTMEHVXXXEESIIXQETYK 21
                                    1 KNTMEHVSSSEESIISQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95GB-0022302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-GB02658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                         03-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYLI-) UNIV LIVERPOOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-272048/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                          WO9716460-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                     Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE17468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                    AAW32220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE17468
                                                                                                       RESULT 5
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Gaps

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91AU-0005706

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19-APR-1991;
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                                                                                                                                                                                                  The invention relates to a composition comprising a peptide or its derivative. The peptide contains an amino acid sequence from alpha-S2 casein precursor. The peptides stimulate the growth of fibroblasts, and thus the synthesis and secretion of collagen. The peptides also stimulate of skin surface. The peptide is useful in the formation and regeneration in the form of a toothpasts or a chewing yum, for alleviating or preventing periodontal disease and a medicament in the form of a cosmetic composition for alleviating or preventing an effect of aging, particularly wrinkling of the skin. The present sequence is bovine alpha-S2 casein precursor protein.
                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                  Use of peptide or its derivative containing an amino acid sequence in alpha-S2 casein precursor in the manufacture of a medicament for alleviating or preventing periodontal disease and an effect of aging in
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Casein; metal ion; dietectic; purification; growth medium; dietary supplement; fertillser.
                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                           95.6%; Score 87; DB 23; Length 222; 81.0%; Pred. No. 4.8e-08.
                                                                                                                                                                                                                                                                                                                                                    Pred. No. 4.8e-08;
); Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR28432 standard; peptide; 21 AA.
                                                                                                                                                                                  Claim 8; Page 6; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anticariogenic phosphopeptide.
                                                                                                                                                                                                                                                                                                                                                                                          16 KNTMEHVSSSEESIISQETYK 36
                                     13-JUN-2001; 2001WO-GB02601.
                                                        30-JUN-2000; 2000GB-0016189
                                                                                                                                                                                                                                                                                                                                                                               1 KNTMEHVXXXEESIIXQETYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92WO-AU00175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                  Local Similarity 81.0 les 17; Conservative
                                                                                                                 WPI; 2002-154690/20.
                                                                            (PEPS-) PEPSYN LTD.
                                                                                                                                                                                                                                                                                                                        222 AA;
 WO200202133-A2.
                    10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-0CT-1992.
                                                                                                Smith JA;
                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR28432;
                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
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The peptide may be prepd. by completely digesting casein in soln. with a proteolytic enzyme, adding mineral acid to the soln. to adjust the pH to 4.7, removing any precipitate, adding calcium chloride to cause aggregation of the peptides in soln. and separating the aggregated phosphopeptides. This method allows prodn. In the phosphopeptide by industrial methods. The phosphopeptide has anticariogenic activity and may be used as a dietectic. The peptide may be used in a microbiological growth medium, as a dietary see also AAR28425-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caries; gingivitis; periodontal disease; osteoporosis; osteomalacia.
                                                                                                                                                        Selected phospho-peptide(s) prodn. having anticariogenic activities etc. - comprises digesting soluble monovalent cation salt of casein in soln., introducing di- or trivalent metal ion and filtering through filter having mol. wt. exclusion limit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 84; DB 13; L. Pred. No. 1.3e-08; 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (VICT-) VICTORIA DAIRY INDUSTRY AUTHORITY.
(UYME-) UNIVERSITY OF MELBOURNE.
(REYN/) EC REYNOLDS.
                       (VICT-) VICTORIAN DAIRY IND AUTHORITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= phosphoserine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                Claim 11; Page 14; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP71322 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KNTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KNTMEHVSSSEESIISEETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.3%;
76.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87WO-AU00172.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
(UYME ) UNIV MELBOURNE
                                                                                                          WPI; 1992-382039/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphopeptide 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                    Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP71322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Seguence
                                                                                                     Query Match
                                                                                                                    Matches
                                                                                                                                                                         RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel phosphopeptides - useful for treating dental diseases, rarefying diseases or diseases relating to malabsorption of minerals
                                                                                                                                                                                                                                                                    caries; gingivitis; periodontal disease; osteoporosis; osteomalacia;
                                   New phosphopeptides contg. defined aminoa cid sequence - useful in treatment of dental, rarefying bone diseases and disease relating to malabsorption of minerals.
                                                                                                                                       Gaps
                                                                                  The phosphopeptide is used in compsns. at a conc. of 0.01-5 wt8. see also AAP71320-P71324.
                                                                                                                                       :
0
                                                                                                                        Score 82; DB 8; Length 20;
Pred. No. 2.9e-08;
                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                      Phosphopeptide #3 for increasing mineral absorption.
                                                                                                                                                                                                                                                                                                                                   /note= "phosphoserine (Pse)"
                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (VICT-) VICTORIAN DAIRY INDUSTRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Column 11; 8pp; English.
                                                                                                                                                                                                            AAR14449 standard; Protein; 20 AA.
                                                                       Claim 6; Page 17; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                   label= OTHER
                                                                                                                                                                                                                                                                                                                                                                         'label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                               /label= OTHER
/note= "Pse"
                                                                                                                                                                                                                                                                                                                             /label= OTHER
                                                                                                                                                                                                                                                                                                                                                         /note= "Pse"
                                                                                                                                                                                                                                                                                                                                                                                 'note= "Pse"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   900S-0563798
                                                                                                                                                                 1 NTMEHVSSSEESIISQETYK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                   90US-0563798
                                                                                                                           90.1%;
80.0%;
                                                                                                                                                         2 NTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYME-) UNIV OF MELBOURNE.
                                                                                                                                                                                                                                            (first entry)
                                                                                                                                  Local Similarity 80.0 nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-316875/43.
                          WPI; 1987-362707/51.
                                                                                                             20 AA;
                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                         US5015628-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1991
                                                                                                                                                                                                                                            10-JAN-1992
             Reynolds EC;
                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                             AAR14449;
                                                                                                              Sednence
                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                   anaemia.
                                                                                                                                            Matches
                                                                                                                                                                                                        AAR14449
ID AAR1
                                                                                                                                                                                               RESULT 9
                                                                                                                                                                                                                             pp
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The peptide may be prepd. by completely digesting casein in soln. with a proteolytic enzyme, adding mineral acid to the soln. to adjust the pH to 4.7, removing any precipitate, adding calcium chloride to cause aggregation of the peptides in soln. and separating the aggregated phosphopeptides. This method allows prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _note= "post-translationally phosphorylated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "post-translationally phosphorylated serine"
This is an example of a highly generic formula for a phosphopeptide of length 5-13 amino acids. The peptides can be made synthetically (e.g. chemical synthesis or genetic engineering) or they can be extracted from cereals, nuts or vegetables or by fractionating a digest of casein, alpha-s-casein, beta-casein or a salt of it. Compositions comprising the peptide may take the form of foodstuff or confectionery, dentifrices; mouthwashes and preparations for topical application to teeth or gingival tissue. The peptides significantly increase absorption of calcium, phosphate and iron in the gut. See AAR14447-R14451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Casein; metal ion; dietectic; purification; growth medium; dietary supplement; fertiliser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    selected phospho-peptide(s) prodn. having anticariogenic activities etc. - comprises digesting soluble monovalent cation salt of casein in soln., introducing di- or trivalent metal ion and filtering through filter having mol. wt. exclusion limit
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                             90.1%; Score 82; DB 12; Length 20; 80.0%; Pred. No. 2.9e-08; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (VICT-) VICTORIAN DAIRY IND AUTHORITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 13; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR28431 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anticariogenic phosphopeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-AU00175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NTMEHVSSSEESIISQETYK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91AU-0005706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYME ) UNIV MELBOURNE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-382039/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
hes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                          20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9218526-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR28431;
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8288888

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Gaps

0;

90.1%; Score 82; DB 14; Length 20; 80.0%; Pred. No. 2.9e-08; 1ve 0; Mismatches 4; Indels

16; Conservative

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Phosphopeptide derived from casein
                                                                                                                                                                                AAR32310 standard; peptide; 20 AA.
                                                                                                      1 NTMEHVSSSEESIISQETYK 20
                                                                                     2 NTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                    10-JUN-1993 (first entry)
                                               Best Local Similarity
                                                                                                                                                                                                             AAR32310:
                                  Query Match
                                                            Matches
                                                                                                                                                      RESULT 12
                                                                                      δ
                                                                                                               QQ
                                                                                                                                                                                                            ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAR32927-35 are casein phosphopeptides which can be used to inhibit dental calculus. These peptides are pref. in the form of salts selected from alkaline metal, alkaline earth metal salts such as Na, Ca, Zh, Cu, Al, K, Sr, Mg and Ni salts. These peptides are pref. present as a Zh/phosphopeptide complex or aggregate. these peptides have anti-calculus potential, and are anti-caries and anti-
of the phosphopeptide by industrial methods. The phosphopeptide has anticariogenic activity and may be used as a dietectic. The peptide may be used in a microbiological growth medium, as a dietary supplement or as a fertiliser. See also AAR28425-33.
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                    Casein; phosphopeptide; dental calculus; salts; alkaline metal; alkaline earth metal; Zn/phosphopeptide complex; aggregate; anti-caries; anti-gingivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Controlling dental calculus by treating teeth with oral compsns. - which contains phospho-peptide(s) having 5-40 amino-acyl
                                                                                                                                                  0;
                                                                                                              90.1%; Score 82; DB 13; Length 20; 80.0%; Pred. No. 2.9e-08; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYME ) UNIV MELBOURNE.
(VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label- Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Phophoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                          AAR32933 standard; Protein; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 19; 23pp; English.
                                                                                                                                                               2 NTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                               1 NTMEHVSSSEESIISQETYK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-0748344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92WO-AU00441
                                                                                                                                                                                                                                                                                                              02-JUL-1993 (first entry)
                                                                                                      Query Match
Best Local Similarity 80.06
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                           Casein phosphopeptide #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1993-093685/11.
                                                                                   20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9303707-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04 - MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                   Sequence
                                                                                                                                                                                                                                                                                       AAR32933;
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The peptide sequence is that of a phosphopeptide prepd. from a tryptic digest of casein. The peptide may be used with an anti-calculus agent, e.g. alkali metal pyrophosphate, in a compsn. for controlling dental tartar. The compsn. inhibits conversion of hyroxyapatite on the teeth. The compsn. is used in the form of a mouthwash, toothpaste, gel, lozenge or chewing gum, for care of the See also AAR32308-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phospho-peptide(s) for dental tartar control - are included in compons. With pyrophosphate(s) or zinc salts to provide good
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                               'note= "post-translationally phosphorylated"
                                                                                                                                                                                                          /note= "post-translationally phosphorylated"
                                                                                                                                                                                                                                                   /note= "post-translationally phosphorylated"
                                                                                                                                                                                                                                                                                                 /note= "post-translationally phosphorylated"
Dental; teeth; tartar control; brushite; calcium phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.1%; Score 82; DB 14; Length 20;
80.0%; Pred. No. 2.9e-08;
Live 0; Mismatches 4; Indels
                        hydroxyapatite; mouthwash; toothpaste.
                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 13; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     92EP-0202024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91GB-0017315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burger AR, Schick LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNIL ) UNILEVER PLC. (UNIL ) UNILEVER NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-060322/08.
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Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AA;
                                                                                                                                    Modified-site
                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                        24-FEB-1993
                                                                                                                                                                                                                                                                                                                                          EP528458-A.
                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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20 AA;

Seguence

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Phosphopeptide; tryptic digestion; sodium caseinate; alpha(s1)-caseinate; phosphoserine; phosphothreonine; phosphotyrosine; phosphohistidine; sugar; sorbito1; mannito1; xylito1; lactito1; cellobilto1; confectionary; caries; gingivitis; calcium; remineralisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ser(P) = post-translationally phosphorylated serine. A mixture of casein phosphopeptides (CPP) and/or their salts may be used in a method for treating dentinal hypersensitivity. Pref. those CPPs contg. the sequence -Ser(P)-Ser(P)-Ser(P)- predominate. The CPPS can be extracted from a casein digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treatment of dentinal hypersensitivity - using casein, component of casein, phospho-protein or phospho-peptide or their salts
                                                                                                                                     Casein phosphopeptide; dentinal hypersensitivity; therapy; tooth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.1%; Score 82; DB 15; Length 20; 80.0%; Pred. No. 2.9e-08;
                                                                                                                                                                                                                                                             /note= "see also residues 8,9,15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sodium caseinate tryptic phosphopeptide T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                            Sequence of casein phosphopeptide (CPP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 16; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR68938 standard; Peptide; 20 AA
                                                                                                                                                                                                                Location/Qualifiers
         AAR47820 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 NTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NTMEHVSSSEESIISQETYK 20
                                                                                                                                                                                                                                                    /label= Ser(P)
                                                                                                                                                                                                                                                                                                                                                                                                        92AU-0003221.
                                                                                                                                                                                                                                                                                                                                                                        93WO-AU00319.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYME ) UNIV MELBOURNE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-025888/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-1995
                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                         29-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                          29-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reynolds EC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus.
                                                                                                                                                                                                                                                                                                        WO9400146-A
                                                                                                                                                                                                                                                                                                                                         06-JAN-1994
                                                                                 21-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR68938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                      Synthetic.
                                                  AAR47820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR68938
AAR47820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAR31237-42 represent phosphopeptides which were used as the active agents in an oral composition. These peptides were stabilised by an anionic polymeric stabiliser. The anionic polymers were chosen from a group consisting of carboxylate anionic polymers polymers, polymers having both a carboxylate and sulfonate moiety, and other such mixtures. The anionic polymeric a sulfonate moiety and other such mixtures. The anionic polymeric stabiliser inhibits destabilisation of the phosphopeptide in the oral source may be used for inhibiting caries and gingivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                           Phosphopeptide; active agent; oral; composition; anionic; polymeric; stabiliser; carboxylate; polymer; sulfonate; destabilisation; fluoride; caries; gingivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oral compsns. contg, a phospho;peptide - with addn. of an anionic polymeric stabiliser to inhibit destabilisation in the oral environment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.1%; Score 82; DB 14; Length 20; 80.0%; Pred. No. 2.9e-08; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                          /label= Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                            label = Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 15; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schick LA;
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                  AAR31239 standard; Protein; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 NTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 NTMEHVSSSEESIISQETYK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92EP-0202023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91US-0731592
                  1 NTMEHVSSSEESIISQETYK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                      18-MAY-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burger AR, Elliott DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-019802/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA;
                                                                                                                                                                                                                         Phosphopeptide 3.
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03-JUL-1992; 17-JUL-1991;

16;

Matches

RESULT 14

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Sequence Query Match

20-JAN-1993.

Modified-site Modified-site Modified-site

Modified-site

Synthetic.

AAR31239;

RESULT 13 AAR31239

qq

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Gaps

; 0

4; Indels

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Peptides (AAR68936-40) are phosphopetides resulting from the tryptic the greation of sodium caselnate. The peptide shown here is derived from alpha(s1), alpha(s2).caselnate (comprising alpha(s2), alpha(s2), alpha(s2), and alpha(s6). The peptides contain the amino phospholistidine, and include in their sequence aspartate and glutamate. The phosphopetides form part of a novel composition containing the sorbitol, mannitol, xylitol, lactitol, collobiitol or mixtures of sorbitol/mannitol or sorbitol/xylitol. The compositions can be used instead of conventional sugars to manufacture confectionary products. The phosphopetides are known to inhibit caries and gingivitis and can act as a source of calcium ions to promote/enhance remineralisation.
                                                                                                                                                                                                                                                                                                                                                 Crystalline poly:ol compositions for use in confectionery and pharmaceuticals - contain a phospho:peptide uniformly distributed within the crystal matrix and can improve oral
                                                    /label= OTHER
/note= "Phosphoserine"
                            'note= "Phosphoserine"
                                                                                                         /note= "Phosphoserine"
                                                                                                                               Disclosure; column 4; 8pp; English.
                /label= OTHER
                                                                                            /label= OTHER
                                                                                                                                                                                                                                                  93US-0078706.
                                                                                                                                                                                                                         94EP-0304083.
                                                                                                                                                                                                                                                                        (ICIL ) ICI AMERICAS INC.
                                                                                                                                                                                                                                                                                                                        WPI; 1995-044845/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 AA;
Modified-site
                                      Modified-site
                                                                           Modified-site
                                                                                                                  Modified-site
                                                                                                                                                                                                                     07-JUN-1994;
                                                                                                                                                                                                                                             16-JUN-1993;
                                                                                                                                                                                            21-DEC-1994.
                                                                                                                                                                     EP629393-A.
                                                                                                                                                                                                                                                                                                Duross JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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0; Gaps 90.1%; Score 82; DB 16; Length 20; 80.0%; Pred. No. 2.9e-08; tive 0; Mismatches 4; Indels Best Local Similarity 80.0 Matches 16; Conservative Query Match δλ

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2 NTMEHVXXXEESIIXQETYK 21 1 NTMEHVSSSEESIISQETYK 20 g

Search completed: February 11, 2003, 18:16:56 Job time : 31.5258 secs

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Sequence 8, Appli
Sequence 6, Appli
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Sequence 6, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
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Sequence 4771, Ap
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                                                                         February 11, 2003, 18:14:31; Search time 10.3918 Seconds (without alignments) 59.459 Million cell updates/sec
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... cgq12_6/ptodata/1/iaa/6A_COMB.pep:*
... cgq12_6/ptodata/1/iaa/6B_COMB.pep:*
... cgq12_6/ptodata/1/iaa/PCTUS_COMB.pep:*
... cgq12_6/ptodata/1/iaa/pcdruS_COMB.pep:*
... cgq12_6/ptodata/1/iaa/pcdruS_COMB.pep:*
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GenCore version 5.1.3
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US-08-954-985A-8

US-08-137-086-8

US-09-066-408-6

US-09-154-985A-7

US-08-154-985A-7

US-08-106-408-12

US-09-066-408-11

US-09-066-408-11

US-09-066-408-11

US-09-066-408-11

US-09-066-408-9

US-09-066-408-9

US-09-066-408-9

US-09-066-408-11

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US-09-066-408-11

US-09-133-44-17

US-09-134-010C-4771

US-09-134-010C-4771

US-09-134-010C-4771

US-09-134-010C-4771

US-09-134-010C-4771

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US-09-136-110

US-09-136-110

US-09-136-110
                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                  262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  - protein search, using sw model
                                                                                                                                       91
1 KNTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                              US-09-380-738A-4
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                             Perfect score:
                                                      OM protein
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                                                                                                                                                         Sequence:
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Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 517, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 37, Appli
Sequence 37, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Patent No. 5256558
                                                              Sequence 1, Appli
Sequence 19, Appl
Sequence 19, Appl
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                                                                                                                                                                                                                                                                                                              US-07-748-344B-8
Sequence 8, Application US/07748344B
Sequence 8, Application US/07748344B
Patent No. 5227154
GENERAL INFORMATION:
APPLICANT: REYNOLDS, ERIC CHARLES
TITLE OF INVENTION: PHOSPHOPEPTIDES FOR THE
TITLE OF INVENTION: TREATMENT OF DENTAL CALCULUS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
US-08-317-401E-2
US-08-317-401E-4
US-09-134-001C-4395
US-08-852-809-4
525658-5
US-08-286-819A-19
US-08-980-357-19
US-08-966-286-8155
US-08-96-357-19
US-08-46-858-155
US-08-48-1515
US-08-46-875-16
US-08-446-875-16
US-08-446-875-16
US-08-446-875-16
US-08-446-875-16
US-08-446-875-16
US-08-875-16
US-08-875-16
US-08-88-207A-317
US-08-88-870-2
US-08-88-870-2
US-08-88-870-317
US-08-88-88-807-3
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL STREET: 100 EAST WISCONSIN AVE., SUITE 1100 CITY: MILWAUKEE
                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 30,492
REFERENCE/DOCKET NUMBER: C.8493-87
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPEY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/748,344B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19910822
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SARA, CIRRLES
REGISTRATION NUMBER: 30,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (608) 255-2022
TELEFAX: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 8:
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STRANDEDNESS: single
TOPOLOGY: linear
    Phosphoserine
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     53202
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7, Appl

Sequence Sequence Sequence

Sequence 3

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LOCATION:
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OTHER INFORMATION: Post-translationally phosphorylated serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Post-translationally phosphorylated serine
                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                       95.6%; Score 87; DB 1; Length 21; 81.0%; Pred. No. 3.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: REYNOLDS, Eric Charles
TITLE OF INVENTION: A Treatment for Sensitive Teeth
TUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Dental School, The University of Melbourne
STREET: 71 Elizabeth Street
                                                                                                                                     Post-translationally phosphorylated serine
                                       Post-translationally phosphorylated serine
                                                                                                                                                                                                                                            Post-translationally phosphorylated serine
                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,985A
FILING DATE: 21-OCT-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362,479
FILING DATE: 22-FEB-1995
ATTORNEY/AGRNT IMPORMATION:
NAME: WOZNY, THOMBAR: 28,922
REFERENCE/DOCKET NUMBER: 28,22-00033
TELECOMMULICATION INFORMATION:
METEROLOGICAL AND APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Melbourne
STATE: Victoria
COUNTRY: Australia
21P: 3000
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08954985A Patent No. 5981475
                                                                                                                                                                                                                                                                                                                                                                                  1 KNTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (414) 271-7590
TELEFAX: (414) 271-5770
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 81.08
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LENGTH: 21
"VPE: Amino Acid
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Gaps
                                               OTHER INFORMATION: Post-translationally phosphorylated serine
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Patent No. 6448374
GENERAL INFORMATION:
APPLICANT: REYNOLDS, ERIC CHARLES
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-translationally phosphorylated serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-translationally phosphorylated serine
                                                                                                                             95.6%; Score 87; DB 2; I
81.0%; Pred. No. 3.4e-10;
Live 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL STREET: 100 EAST WISCONSIN AVE., SUITE 1100 CITY: MILWAUKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                    1 KNTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                       1 KNTMEHVSSSEESIISQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (608) 255-2022
(608) 255-2182
                                  NAME/KEY: Phosphoserine LOCATION: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAR-1994
                                                                                                                                               Best Local Similarity 81.0 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STATE: WISCONSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53202
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                                                                                                                             Query Match
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Best Local Similarity 81.0%; Pr. Matches 17; Conservative 0;
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APPLICANT: Wilkinson, Mark Charles
APPLICANT: Wilkinson, Mark Charles
APPLICANT: Liu, Oing-Ming
TITLE OF INVENTION: Casein Fragments Having Growth Promoting
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.6%; Score 87; DB 3; Length 222;
                                                                                                                                                                                           Query Match

95.6%; Score 87; DB 4; Length 21;
Best Local Similarity 81.0%; Pred. No. 3.4e-10;
Matches 17; Conservative 0; Mismatches 4; Indels
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                               Post-translationally phosphorylated serine
                                                                                                                                   Post-translationally phosphorylated serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPALIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29,684
FP: 018317-000100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/066,408
FILING DATE: 13-MAR-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB96/02658
FILING DATE: 31-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9522302.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 31-OCT-1995
ATTORREY/AGENT INFORMATION:
NAME: DOW. KATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor"
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Patent No. 6060448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                    1 KNTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                 1 KNTMEHVSSSEESIISQETYK 21
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                           Phosphoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..222
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                            US-08-137-086-8
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                                                                           FEATURE:
FEATURE:
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Query Match

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                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: REINOLDS, ERIC CHARLES
APPLICANT: REINOLDS, ERIC CHARLES
TITLE OF INVENTION: PHOSPHOPEPTIDES FOR THE
TITLE OF INVENTION: TREATMENT OF DENTAL CALCULUS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL
STREET: 100 EAST WISCONSIN AVE., SUITE 1100
Pred. No. 4.4e-09;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.8493-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/07/748,344B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                  ; Sequence 7, Application US/07748344B
; Patent No. 5227154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                            16 KNTMEHVSSSEESIISQETYK 36
                                                       1 KNTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (608) 255-2022
TELEFAX: (608) 255-2182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US
FILING DATE: 19910822
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 26832 ANDSTARK INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19910822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
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MEDIUM TYPE: FLOPPY
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                                                                                                                                                                                                                                                                                                                                                                                           STATE: WISCONSIN
                                                                                                                                                                                                                                                                                                                                                                           MILWAUKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  53202
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US-07-748-344B-7
                                                                                                                                                                   US-07-748-344B-7
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH:
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FEATURE:
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TELEFAX: (608) 255-218;
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: Protein
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                                                                                                                                                                                                                                                                WISCONSIN
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                                                                                                                                                                                                                                           CITY: MILWAUKEE
STATE: WISCONSIN
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                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                 53202
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                                                                                                                                                                                                                                                                              COUNTRY:
                                                 RESULT 7
US-08-137-086-7
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US-08-137-086-7
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   90.1%; Score 82; DB 1; Length 20; Conservative 0; Mismatches 4; Indels
                                          4; Indels
                                                                                                                                                                                          Sequence 7. Application US/08954985A
Patent No. 5981475
GENERAL INFORMATION:
APPLICANT: REYNOLDS, Eric Charles
TITLE OF INVENTION: A Treatment for Sensitive Teeth
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dental School, The University of Melbourne
STREET: 711 Elizabeth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.1%; Score 82; DB 2; Length 20; 80.0%; Pred. No. 2.9e-09; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: WOZNY, Thomas M
REGISTRATION NUMBER: 28,922
REFERENCE/DOCKET NUMBER: 322-00033
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Ascii
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/954,985A
FILING DATE: 21-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM
OPERATING SYSTEM: Windows 95
                                                                                          1 NTMEHVSSSEESIISQETYK 20
                                                                      2 NTMEHVXXXEESIIXQETYK 21
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TELEFAX: (414) 271-5770
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskette
COMPUTER: IBM
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                                                                                                                                                                                                                                                                                                                                                        COUNTRY: Victoria
COUNTRY: Australia
2IP: 3000
Query Match
Best Local Similarity
Matches 16; Conserv
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TOPOLOGY: Linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  STREET: 711 ELLE
CITY: Melbourne
                                                                                                                                                          RESULT 6
US-08-954-985A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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APPLICANT: REYNOLDS, ERIC CHARLES
TITLE OF INVENTION: PRODUCTION OF PHOSPHOPEPTIDES FROM CASEIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                     ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL STREET: 100 EAST WISCONSIN AVE., SUITE 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY TAGENT INCORMATION:
NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: C.8493-87
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,086
FILING DATE: 04-MAR-1994
CLASSIFICATION: 530
PRIOR APPLICATION: AFA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
; Sequence 7, Application US/08137086
; Patent No. 6448374
                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (608) 255-2022
TELEFAX: (608) 255-2182
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Sequence 7, Application US/09066408

Sequence 7, Application US/09066408

GENERAL INFORMATION:

APPLICANT: Smith, John Arthur

APPLICANT: Wilkinson, Mark Charles

APPLICANT: Liu, Oling-Ming

TITLE OF INVENTION: Casein Fragments Having Growth Promoting

TITLE OF INVENTION: ACLIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.9%; Score 54.5; DB 3; Length 223; 59.1%; Pred. No. 0.0061; tive 1; Mismatches 7; Indels 1
APPLICANT: Liu, Qing-Ming
TITLE OF INVENTION: Caselin Fragments Having Growth Promoting
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "sheep alpha-S2 casein
                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,408 FILING DATE: 13-MAR-1998 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Two Embarcadero Center, Eighth Floor
San Francisco
California
                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 018317-000100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB96/02658
FILING DATE: 31-OCT-1996
FILING DATE: 31-OCT-1996
FILING DATE: 31-OCT-1995
FILING DATE: 31-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Dow, Karen B. REGISTRATION NUMBER: 29,684
                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 223 amino acids TYPE: amino acid
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Best Local Similarity 59.1'
Matches 13; Conservative
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CTHER INFORMATION: F
US-09-066-408-11
                                                                                                                                                San Francisco
California
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STATE: Ci
COUNTRY:
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                                                                                                                                                                                         COUNTRY:
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                                                                                                       Sequence 12, Application US/09066408

Patent No. 606048

GENERAL INFORMATION:
APPLICANT: Smith, John Arthur
APPLICANT: Liu, Qing-Ming
TITLE OF INVENTION: Casein Fragments Having Growth Promoting
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.4%; Score 59.5; DB 3; Length 235; 63.6%; Pred. No. 0.00073; Live 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "pig alpha-S2 casein
precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/066,408
                                                                                                                                                                                                                                                                                                                      SEE: Townsend and Townsend and Crew LLP: Two Embarcadero Center, Eighth Floor California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 018317-000100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
IELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARATTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PREDICATION NUMBER: WO PCT/GB96/02658
FILING DATE: 31-0CT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-1998
13-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/09066408
Patent No. 6060448
GENERAL INFORMATION:
APPLICANT: Smith, John Arthur
APPLICANT: Wilkinson, Mark Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: GB 9522302.0 FILING DATE: 31-OCT-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KNTMEHVXXXEESI-IXQETYK 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Dow, Karen B. REGISTRATION NUMBER: 29,684
                   1 NTMEHVSSSEESIISQETYK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 63.6
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: ; OTHER INFORMATION: ; G19-066-408-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                              94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                     US-09-066-408-12
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APPLICANT: Smith, John Arthur
APPLICANT: Wilkinson, Mark Charles
APPLICANT: Wilkinson, Mark Charles
APPLICANT: Wilkinson, Mark Charles
APPLICANT: Liu, Qing-Ming
TITLE OF INVENTION: Casein Fragments Having Growth Promoting
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STRET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.8%; Score 53.5; DB 3; Length 223; 59.1%; Pred. No. 0.0094; iive 1; Mismatches 7; Indels :
COMPUTER REAGABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/09/066,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , LUCATION: 1..223
; OTHER INFORMATION: /note= "goat alpha-S2 casein
; OTHER INFORMATION: precursor allele A"
US-09-066-408-7
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CURRENT APPLICATION DATA:
FPLICATION NUMBER: US/09/066,408
FILING DATE: 13-MAR-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 018317-000100US TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  APPLICATION NUMBER: US/09/066,408
FILING DATE: 13-MAR-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB96/02658
FILING DATE: 31-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9522302.0
FILING DATE: 31-OCT-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09066408
Patent No. 6060448
                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
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Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94111-3834
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APPLICANT: Smith, John Arthur
APPLICANT: Wilkinson, Mark Charles
APPLICANT: Liu, Oing-Ming
TITLE OF INVENTION: Casein Fragments Having Growth Promoting
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.8%; Score 53.5; DB 3; Length 223; 59.1%; Pred. No. 0.0094; ive 1; Mismatches 7; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , LUCATION: 1..223
; OTHER INFORMATION: /note= "goat alpha-S2 casein
; OTHER INFORMATION: precursor allele B"
US-09-066-408-8
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PatentIn Release #1.0, Version #1.30
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                         018317-000100US
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REFERENCE/DOCKET NUMBER: 018317-000100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5,09/066,408
FILING DATE: 13-MAR.1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB96/02658
FILING DATE: 31-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9522302.0
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB96/02658
FILING DATE: 31-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9522302.0
FILING DATE: 31-0CT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                      NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 0183:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 9, Application US/09066408
; Patent No. 6060448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KNTMEHVXXXEESI-IXQETYK 21
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                                                                                                                                                                                                                                                                                                                                    LENGTH: 223 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 31-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 58.8%
Best Local Similarity 59.1%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
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; Sequence 4, Application US/09086662; Patent No. 5962264; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                             Pennsylvania
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hes 7; Conserva
                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Human
US-09-734-673-2
                                                                                                                                                                                                                                                                                  USA
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LENGTH: 436
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US-09-086-662-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
TITLE OF INVENTION: BACILLUS THURINGIENSIS apr AND npr
TITLE OF INVENTION: PROTEASE GENES AND ALKALINE PROTEASE DEFICIENT AND NEUTRAL
TITLE OF INVENTION: PROTEASE DEFICIENT B.T. STRAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                    58.8%; Score 53.5; DB 3; Length 223; 59.1%; Pred. No. 0.0094;
Live 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.2%; Score 42; DB 1; Length 566; 40.0%; Pred. No. 3.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel, P.C.
ADDRESSEE: A S. Nadel
STREET: 1601 Market Street, 36th floor
                                                                                                                                                                                            , LUCATION: 1..223
; OTHER INFORMATION: /note= "goat alpha-S2 casein
; OTHER INFORMATION: precursor allele C"
US-09-066-408-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/415,823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08415823
Patent No. 5759538
   TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                               1 KNTMEHVXXXEESI-IXQETYK 21
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 566 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                             Best Local Similarity 59.1
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-415-823-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
'.hog 8; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Philadelphia STATE: Pennan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19103-2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                              STRANDEDNESS:
                                                                                                                                                   IOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-415-823-4
                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
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APPLICANT: Donovan, William P.
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
TITLE OF INVENTION: BACILLUS THURINGIENSIS APP AND NPT
TITLE OF INVENTION: PROTESASE GENES AND ALKALINE PROTESASE DEFICIENT AND NEUTRA:
TITLE OF INVENTION: PROTESASE DEFICIENT B.T. STRAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CLOOM 2000 CURRENT APPLICATION NUMBER: US/09/734,673 CURRENT FILING DATE: 2000-12-13 NUMBER OF SEO ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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Pred. No. 16;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.2%; Score 42; DB 2; Length 566; 40.0%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel, P.C. c/o
ADDRESSEE: A.S. Nadel
STREET: 1601 Market Street, 36th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/086,662
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/415,823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09734673 Patent No. 6410294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 NTIDHVTNDDKSPVKQEAPK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
, APPLICANT: GUEGLER, Karl et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 NTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          566 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 46.2%
Best Local Similarity 40.0%
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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1 KNTMEHVXXXEESI 14

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Search completed: February 11, 2003, 18:22:10 Job time : 11.5918 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments)
52.729 Million cell updates/sec February 11, 2003, 18:19:51; Search time 10.1753 Seconds Run on:

US-09-380-738A-4

91 1 KNTMEHVXXXEESIIXQETYK 21 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

140259 segs, 25548876 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/DSO6_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					COLUMNICO	
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Result	Score	Query	Query Match Length DB	DB	ID	Description
				1		1
٦	37	40.7	121	10	US-09-741-669-447	Sequence 447, App
8	37	40.7	879	φ	US-10-108-605-217	Sequence 217, App
e	36	39.6	999	10	US-09-815-242-13637	Seguence 13637, A
4	36	39.6	949	10	US-09-815-242-13513	Sequence 13513, A
Ŋ	35	38.5	54	10	US-09-864-761-47515	Sequence 47515, A
9	35	38.5	415	10	US-09-815-242-12593	Sequence 12593, A
7	35	38.5	415	10	US-09-815-242-12909	Sequence 12909, A
8	35	38.5	487	10	US-09-815-242-5509	Sequence 5509, Ap
o	35	38.5		12	US-10-028-780-2	Seguence 2, Appli
10	35	38.5		10	US-09-925-300-1626	Sequence 1626, Ap
11	34	37.4	1116	10	US-09-790-318-2	Sequence 2, Appli
12	33.5	36.8		6	US-09-738-626-3894	Sequence 3894, Ap
13	33	36.3		10	US-09-925-301-1302	Sequence 1302, Ap
14	33	36.3		10	US-09-789-919-48	Sequence 48, Appl
15	33	36.3		10	US-09-764-898-197	Sequence 197, App
16	32	35.2	154	6	US-09-738-626-5286	Sequence 5286, Ap
17	32	35.2		10	US-09-815-242-13500	Sequence 13500, A
18	32	35.2		10	US-09-952-013A-4	Sequence 4, Appli
19	32	35.2	740	10	US-09-815-242-10876	Sequence 10876, A

	13083,		Sequence 12610, A	Sequence 12996, A	Sequence 11411, A	11573,	Sequence 1684, Ap		a .	Sequence 2, Appli	Sequence 4, Appli	-	Sequence 19, Appl	Sequence 23, Appl	Sequence 501, App	Sequence 7, Appli	Sequence 472, App	Sequence 13666, A	N.	Sequence 9, Appli		Sequence 442, App	Sequence 442, App	Sequence 442, App	Sequence 442, App	
US-09-815-242-5885	US-09-815-242-130	US-09-815-242-5639	US-09-815-242-1261	US-09-815-242-1299	US-09-815-24	US-09-815-24	US-09-925-301-1	US-09-922-199A-26	US-09-971-228-9	US-09-771-063-2		US-09-842	US-09-731-	US-10-037-616	US-09-925-	0-S0	US-09-925-302-47	US-09-815-242-13666	0S-0	US-10-036-041-9	US-10-035-855-9	174-590-44	US-10-176-758-442	-175 - 737 - 44	US-10-173-706-442	
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1029	104	208	579	628	16	16	16	17	35	35	35	35	35	35	35	39	39	41	43	44	44	44	440	44	44	
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32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	
20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	800	36	4.0	4.1	42	£ 7	44	4 5	

ALIGNMENTS

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            Sequence 447, Application US/09741669
Sequence 447, Application US/09741669
Patent No. US2002002718A1
GENERAL INFORMATION:
APPLICANT: POLISEN, Rari L.
APPLICANT: Ohlsen, Rari L.
APPLICANT: Opien, Parith W.
TITLE OF INVENTION: proliferation of E. coli
FILE REFRENCE: ELIFRA.009A
CURRENT FILING DATE: 2000-12-19
PRIOR PILING DATE: 1999-12-23
NUMBER OF SED ID NOS: 481
SOFTWARE: FastSED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 217, Application US/10108605
; Patent No. US20020160934A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 KLQMQHVDPSQENIVVQK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KNTMEHVXXXEESIIXQE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Escherichia coli
US-09-741-669-447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 38.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-108-605-217
US-09-741-669-447
                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 447
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
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Gaps

APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Ramdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT EN

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TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
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APPLICANT: Haselbeck, Robert

APPLICANT: Oblsen, Kari L.

APPLICANT: John J.

APPLICANT: Zysind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Yamamoto, Robert T.

PRICANT: John D.

PRICANT: John Date: 2001-03-21

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,931

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,931

PRIOR APPLICATION NUMBER: 60/253,931

PRIOR FILING DATE: 2001-12-20

PRIOR PRIOR APPLICATION NUMBER: 60/253,038

PRIOR FILING DATE: 2001-12-20

PRIOR PRIOR APPLICATION NUMBER: 60/253,038

PRIOR PRIOR APPLICATION NUMBER: 60/250,308

PRIOR APPLICATION NUMBER: 60/250,308

PRIOR APPLICATION NUMBER: 60/250,308

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PRIOR APPLICATION NUMBER: 60/250,308

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PRIOR APPLICATION NUMBER: 60/250,308

PRIOR APPLICATION NUMBER: 60/250,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.7%; Score 37; DB 9; Length 879; 38.1%; Pred. No. 42; tive 4; Mismatches 9; Indels
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                              FILE REFERENCE: 31133B
CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: Patentin Ver: 2.1
SOFTWARE: 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13637, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-108-605-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  693 KHVVEQVHEEQERIVKLETIK 713
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Best Local Similarity 38.15
Matches 8; Conservative
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Best Local Similarity
7; Conserva
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LENGTH: 666
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; Sequence 47515, Application US/09864761
; Batent No. US2020048763A1
; Batent No. US20202048763A1
; APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Penn, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL I
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; TITLE OF INVENTION UNMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR PAPLICATION NUMBER: US 60/207,456
; PRIOR PAPLICATION NUMBER: US 99/632,366
; PRIOR PAPLICATION NUMBER: GB 24263.6
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR APPLICATION NUMBER: US 60/236,359
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                                                                                                                                                                                                                                                                               APPLICANT: Yananoto, Robert T.
APPLICANT: Yananoto, Robert T.
APPLICANT: Xu, H. Howard
ITILE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 05/99/815,242
CURRENT FILING DATE: 2001.03.21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000.03.23
PRIOR FILING DATE: 2000.05.23
PRIOR PRICATION NUMBER: 60/205,848
PRIOR FILING DATE: 2000.10.23
PRIOR PILICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000.11.27
PRIOR PILING DATE: 2000.11.27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000.11.27
PRIOR FILING DATE: 2000.11.27
PRIOR FILING DATE: 2000.11.27
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PRIOR FILING DATE: 2000.11.27
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PRIOR FILING DATE: 2000.11.27
PRIOR FILING DATE: 2000.11.27
PRIOR FILING DATE: 2000.12.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.6%; Score 36; DB 10; Length 676; 33.3%; Pred. No. 48;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                 Sequence 13513, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Streptococcus pneumoniae US-09-815-242-13513
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                                                                                                                                                                        Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                                                                       GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                                                                  Carr, Grant J.
                                                                                                                                                   Ohlsen, Kari
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US-09-815-242-13513
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LENGTH: 676
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APPLICANT:
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TYPE: PRT
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.1

OTHER INFORMATION: EST_HUMAN HIT: AL040793.1, EVALUE 8.00e-24

OTHER INFORMATION: SWISSPROT HIT: Q39565, EVALUE 2.70e+00

US-09-864-761-47515
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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3; Mismatches
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                          PRIOR FILING DATE: ZUCUCUSO PRIOR PALLICATION NUMBER: PCT/USO1/00666 PRIOR APPLICATION NUMBER: PCT/USO1/00667 PRIOR PLING DATE: 2001-01-30 PRIOR PLING DATE: 2001-01-30 PRIOR PLING DATE: 2001-01-30 PRIOR PLING DATE: 2001-01-30 PRIOR PELICATION NUMBER: PCT/USO1/00669 PRIOR PELING DATE: 2001-01-30 PRIOR PLING DATE: 2000-09-21 PRIOR PLING DATE: 2000-09-21 PRIOR PLING DATE: 2000-09-21 PRIOR PLING DATE: 2000-09-20 PRIOR PLING DATE: 2000-09-20 PRIOR PLING DATE: 2000-09-20 PRIOR PLING DATE: 2000-09-20 PRIOR PLING DATE: 2000-09-20 PRIOR PLING DATE: 2000-09-20 PRIOR PLING DATE: 2000-09-20 PRIOR PLING DATE: 2000-09-20 PRIOR PLING DATE: 2000-09-20 PRIOR PLING DATE: 2000-09-20 PRIOR PLING DATE: 2000-09-20 PRIOR PLING DATE: 2000-09-20 PRIOR PLING DATE: 2000-09-20 PRIOR PLING DATE: 2000-09-20 PRIOR PRIOR PLING DATE: 2000-09-20 PRIOR PRIOR PLING DATE: 2000-09-20 PRIOR PRIOR PLING DATE: 2000-09-20 PRIOR PRIOR PLING DATE: 2000-09-20 PRIOR PRIOR PLING DATE: 2000-09-20 PRIOR PRIOR PLING DATE: 2000-09-20 PRIOR PRIOR PRIOR PRIOR PRIOR PLING DATE: 2000-09-20 PRIOR PRIOR PRIOR PRIOR PRIOR PLING DATE: 2000-09-20 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR P
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
           FILING DATE: 2000-09-27
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Matches 6; Conservative
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LENGTH: 54
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APPLICANT:
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APPLICANT:
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Pred. No. 43;
4; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dissen, Karl L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFRENCE: ELITRA.011A
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12593
LENGTH: 415
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
                     PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
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Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Staphylococcus aureus US-09-815-242-12593
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33.3%;
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FILING DATE: 2000-05-26
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APPLICANT: Haselbeck, Robert
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.5%; Score 35; DB 10; Length 487; 33.3%; Pred. No. 52;
                                                                                                                                   APPLICANT: ADSELDECK, KODELL
APPLICANT: Oblisen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PECKATYOTES
FILE REFERENCE: ELITRA, 0.11A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/201,078
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PRIOR FILING DATE: 2000-05-23
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PRIOR FILING DATE: 2000-11-27
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PRIOR PILING DATE: 2000-11-27
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                        Sequence 5509, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHILATIFARD, ALI
CONAWAY, JOAN W.
CONAWAY, RONALD C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 2, Application US/10028780
; Patent No. US20020132329Al
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 34
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Best Local Similarity 33.3.
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COUNTRY: USA
ZIP: 20005-3934
US-09-815-242-5509
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LOCATION: (11)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (544)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids \mathtt{NAME/KEY}\colon \mathtt{SITE}
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FILE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
SOFTWARE: PACENTIN VOMBER: 60/124,270
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PACENTIN VET. 2.0
SEQ ID NO 1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 38.5%; Score 35; DB 12; Length 640; Similarity 42.1%; Pred. No. 70; 8; Conservative 3; Mismatches 8; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/028,780
FILING DATE: 28-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/026,343
FILING DATE: «Unknown-
FILING DATE: «Unknown-
APPLICATION NUMBER: US 60/038,447
FILING DATE: 19-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: GOLOSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1488.0880001
TELEPOMUNICATION INFORMATION:
TELEFAX: (202) 372-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENX: (202) 372-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENX: AND AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND ADDRESS AND
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; Patent No. US20020111681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TMEHVXXXEESIIXQETYK 21
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US-09-925-300-1626
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38.5%; Score 35; DB 10; Length 677;

Query Match

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Sequence 48, Application US/09789919
; Sequence 48, Application US/09789919
; Patent No. US200064855A1
; GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor
APPLICANT: MOOFF, Kater
ITILE OF INVENTION: GELES THAT REGULATE HEMATOPIETIC BLOOD FORMING STEM
ITILE OF INVENTION: CELLS AND USES THEREOF
FILE REFERENCE: 2275-1-005
CURRENT APPLICATION NUMBER: US/09/789,919
CURRENT FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 96
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Sequence 1302, Application US/09925301
Setent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR FILING DATE: 1909-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
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                    7; Indels
Best Local Similarity 47.4%; Pred. No. 67;
Matches 9; Conservative 2; Mismatches
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; Patent No. US20020090673A1
; GENERAL INFORMATION:
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                                                                                          12 NRCEHLERTIESILNQ-TY 29
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Best Local Similarity 33...
Rest Local Similarity 33...
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US-09-925-301-1302
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US-09-925-301-1302
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LENGTH: 565
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LENGTH: 693
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                                                                     δy
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Patent No. US20020038012A1
GENERAL INFORMATION:
APPLICANT: Boroho, Gregory
APPLICANT: Scoville, John
APPLICANT: Zambrowicz, Brian
ATILE OF INVENTION: No. US20020038012A1e1 Human Regulatory Protein and Polynucleotide
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                                    8; Indels
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/37484
PRIOR PLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
             42.1%; Pred. No. 74; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/790,318 CURRENT FILING DATE: 2001-02-21 PRIOR APPLICATION NUMBER: US 60/184,015 PRIOR FILING DATE: 2000-02-22 NUMBER OF SEQ ID NOS: 3 SOFTWARE: FastSEQ for Windows Version 4.0
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ANDO, SEIKO
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APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, PANIO
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                                                                              3 TMEHVXXXEESIIXQETYK 21
                                                                                                                     65 TVLHVKLTETAIRALETYQ 83
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SOFTWARE: PatentIn ver. 3.0
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Matches 7; Conservative
                  Best Local Similarity 42.19
Matches 8; Conservative
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LENGTH: 345
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LENGTH: 1116
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Query Match

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### APPLICANT: Rosen et al.
### TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
### TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
### CURRENT APPLICATION NUMBER: US/09/764,898
### CURRENT FILING DATE: 2001-01-17
### PRIOR PAPILCATION data removed - consult PALM or file wrapper
### SOFTWARE: Patentin Ver. 2.0
### SOFTWARE: Patentin Ver. 2.0
### SOFTWARE: Patentin Ver. 2.0
### SOFTWARE: Patentin Ver. 2.0
### CONSONISM: Homo sapiens
### US ON 197
### CONSONISM: Homo sapiens
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1. /cgn2_6/ptodata/1/paa/PCTUS_CONB.pep:*
2. /cgn2_6/ptodata/1/paa/USO6_COMB.pep:*
3. /cgn2_6/ptodata/1/paa/USO7_COMB.pep:*
4. /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*
5. /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*
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7. /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*
8. /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*
9. /cgn2_6/ptodata/1/paa/USO85_COMB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                       4569144 seqs, 644733110 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum Match 100%
Listing first 45 summaries
                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                            1 KNTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 4, Appli	Sequence 3, Appli	Sequence 1509, Ap	Sequence 1509, Ap	Sequence 47481, A	Sequence 533, App
SUMMARIES		D	17 US-09-380-738A-4	US-07-731-592B-3	US-09-573-655A-1509	US-09-573-655B-1509	PCT-US01-08631-47481	PCT-US01-42950-533
		DB		m	19	19	Н	,
		Query Match Length DB ID	1 1 1	20	279	279	408	921
	æ	Query Match	91.2	90.1	49.5	49.5	47.3	47 3
		Score	83	82	4.5	45	43	13
		Result No.	-	0	۰,	4		9 (4

LOCATION: (8)...(8)
OTHER INFORMATION: Xaa is a phosphorylated Serine
NAME/KEY:
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa is a phosphorylated Serine
NAME/KEY: misc_feature
LOCATION: (10)...(10)
OTHER INFORMATION: Xaa is a phosphorylated Serine
OTHER INFORMATION: Xaa is a phosphorylated Serine

ORGANISM: Bos sp.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (8)..(8)

TYPE: PRT

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13	39.5	43.4	339	18	US-09-438-185-1049	Sequence 1049, Ap
14	6	~	339	18	US-09-438-185A-10	1049,
15	39	ς.	409	22	US-09-897-516-640	0400
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21	38			21	US-09-764-874-343	500
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					ALIGNMENTS	
RESHLT 1						
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S.	ce 4, A	pplica	ation US	60/	380738A	
GENERA	L INFOR	MATION	ENERAL INFORMATION:			
)	CANT: R	EYNOLI	S, Eric	•		
	OF INV	INVENTION: C.	N: CALCIUM	MD:	PHOSPHOPEPTIDE COMPLEXES	
; FILE REFER	REFEREN	CE: 07	10268/03	_	KOCL 0007 007	
	NT APPL	ICALL	ON NUMBE	7	5/09/300,730	
	TTTT IN	NG DA	APPLICATION NIMBER.	, D	r/AII98/00160	
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DETOR	APPLICATION NUMBER	ATTON	NUMBER		PO5662	
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NUMBE	R OF SE	QIO	NOS: 23			
SOFIW	ARE: Pa	PatentIn	n versi	ion 3	0.	
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                                                                                                 91.2%; Score 83; DB 17; Length 21; 100.0%; Pred. No. 6.7e-09; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: POSt-translationally phosphorylated OTHER INFORMATION: serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Post-translationally phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COTHER INFORMATION: Serine

OTHER INFORMATION: Serine
US-07-731-5928-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: POSt-translationally phosphorylated OTHER INFORMATION: serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.1%; Score 82; DB 3; Length 20; 80.0%; Pred. No. 1e-08; 1ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette-3.5 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Burger, Allan R.
APPLICANT: Elliott, David L.
APPLICANT: Schick, Laura A.
TITLE OF INVENTION: Oral Compositions Containing
TITLE OF INVENTION: Phosphopeptide
NUMBER OF SEQUENCES: SCHESPONDENCE ADDRESS:
: NAME/KEY: misc_feature

: LCCATION: (16)..(16)

: OTHER INFORMATION: Xaa is a phosphorylated Serine

US-09-380-738A-4
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/731,592B
FILING DATE: 19910717
                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/07731592B GENERAL INFORMATION:
                                                                                                                                                                                                1 KNTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                           1 KNTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19910717
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                            Query Match
Best Local Similarity 100.C
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: AMINO ACID
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 80.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PS/2
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 45 Rive:
CITY: Edgewater
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
                                                                                                                                                                                                                                                                                           US-07-731-592B-3
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RESULT 3
US-09-573-655A-1509
Sequence 1509, Application US/09573555A
Sequence 1509, Application US/0957355A
Sequence 1509, Application US/0957355A
SEQUENCE INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypept
TITLE OF INVENTION: Thereby
CURRENT FILEND NUMBER: US/09/573,655A
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 3280
SOCTHARE: PatentIn Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SOLOVEEV, Victor and TROUKHAN, Maxim
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypepti
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-0876p
CURRENT APPLICATION NUMBER: US/09/573,655B
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 3281
SOFTWARE: Patentin version 3.0
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41.2%; Pred. No. 6.4;
tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 1
Pred. No. 6.4;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US01-08631-47481; Sequence 47481, Application PC/TUS0108631; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1509, Application US/09573655B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Arabidopsis thaliana
1 NTMEHVSSSEESIISQETYK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.5%;
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1509
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42.1%; Pred. No. 76;
tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.3%; Score 43; DB 1; Length 921;
                                                                                                              DB 1; Length 408;
                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 21272-096
CURRENT APPLICATION NUMBER: PCT/US01/42950
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILLE REFERENCE: 21272-096
CURRENT APPLICATION NUMBER: PCT/US01/42950
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 09/714,936
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                            Ouery Match

47.3%; Score 43; DB

Best Local Similarity 42.1%; Pred. No. 26;

Matches 8; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US01-42950-532; Sequence 532, Application PC/TUS0142950; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             ; Sequence 533, Application PC/TUS0142950 ; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.18;
                                                                                                                                                                                                                      |: || | || :: || 253 TVNHVRFSENEIIIEDDYK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TMEHVXXXEESIIXQETYK 21
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                        ; ORGANISM: Homo sapiens
PCT-US01-08631-47481
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US-09-791-537-91913
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; SEQ ID NO 47481
; LENGTH: 408
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LENGTH: 942
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LENGTH: 921
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                                       TYPE: PRT
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APPLICANT: Bloomix, Inc.
APPLICANT: Bloomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERFENCE: 251/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILINO DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEC TO NO 91913
LENGTH: 566
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APPLICANT: BODOMIX, INC.
APPLICANT: BODOMIX, INC.
APPLICANT: Debc, Derek
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APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICANTION NUMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PALCALL NO VERSION 3.0
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US-09-328-352-5117
US-09-328-352
Sequence 5117, Application US/09328352
Sequence 5117, Application US/09328352
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBA;
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 46.2%; Score 42; DB 21; Length 566; Best Local Similarity 40.0%; Pred. No. 63; Matches 8; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 125976, Application US/09791537; GENERAL INFORMATION:
Sequence 91913, Application US/09791537 GENERAL INFORMATION:
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US-09-328-352-5117
                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Bacillus thuringiensis US-09-791-537-91913
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Best Local Similarity 40.0
Matches 8; Conservative
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US-09-791-537-125976
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LENGTH: 566
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APPLICANT: Spiridanow, Sergei
TITLE OF INVENTION: Xenorhablus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)B
                                                                                                                                                                                                                                                                                                                                                                                                              1;
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45.0%; Pred. No. 1e+02;
tive 4; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 43.4%; Score 39.5; DB 18; Length 339; Best Local Similarity 45.0%; Pred. No. 1e+02; Matches 9; Conservative 4; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
APPLICANT: Ralman, Sue
APPLICANT: Talman, Sue
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REPERENCE: 018941-000411US
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR PILING DATE: 1998-11-12
PRIOR PILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FEALESQ for Windows Version 3.0
               CURRENT APPLICATION NUMBER: US/09/438,185
CURRENT FILING DATE: 1999-11-11
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1049
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GENERAL INPORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Hintle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Krasomil-Osterfeld, Karina
                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-438-185-1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Chlamydia pneumoniae
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                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 45.0%
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: CPn1048
US-09-438-185A-1049
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US-09-897-516-6405
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LENGTH: 339
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GENERAL INFORMATION:

APPLICANT: Gary L. Breton

TITLE OF INVENTION:

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: US/09540,209B

CURRENT FILING DATE: 2000-01-04

CURRENT FILING DATE: 2000-04-04

SEQ ID NO 8326

LENGTH: 861
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GEMERAL INFORMATION:
APPLICANT: Griffais, F.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT PILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NOS: 6849
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Query Match 45.1%; Score 41; DB 17; Length 187; Best Local Similarity 42.9%; Pred. No. 24; Matches 9; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.0%; Score 40; DB 19; Length 861;
42.1%; Pred. No. 2.7e+02;
Live 4; Mismatches 7; Indels
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The Regents of the University of California VENTION: Chlamydia Pneumoniae Genome Sequence:NCE: 018941-000411US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 43.4%; Score 39.5; I Best Local Similarity 45.0%; Pred. No. 86; Matches 9; Conservative 4; Mismatches
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                                                                                                                        101 KNSEEDFKTKEESILLNDTLK 121
                                                                                            1 KNTMEHVXXXEESIIXQETYK 21
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ORGANISM: Chlamydia pneumoniae
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Mitchell, Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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US-09-540-209B-8326
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Matches 8; Conserv
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TITLE OF INVENTION:
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APPLICANT:
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(without alignments) 72.734 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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1 KNTMEHVXXXEESIIXQETYK 21
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                      Sequence:
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Pending_Patents_AA_New:*

: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

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: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 63963, A Sequence 2, Appli Sequence 2, Appli Sequence 48, Appli Sequence 52616, A Sequence 52629, A Sequence 52639, A Sequence 70693, A Sequence 70 52618, A 52618, A 70693, A 70693, A 4756, Ap 5000, Ap Description Sequence S PCT - USG2 - 21361 - 48 US-10-188 - 186 - 48 US-09-724-676-52616 US-09-724-676-52629 US-09-724-676-52629 US-09-724-676-52639 US-09-724-676-76-52639 US-09-724-676-76-52639 US-09-724-676-76-52639 US-09-724-676-76-52639 US-09-724-676-76-52639 US-09-724-676-76-52639 US-10-218-140-5000 US-09-724-676-63963 US-09-724-676A-63963 US-10-103-140-2 Match Length DB 411.8 411.8 411.8 410.7 440.7 Query Score 2223109845222310988744 Result N_o

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0-170-385-99 9-134-000C-5441 99-9134-000C-5441 99-950-084-6869 9-724-676-58692 99-724-676-58691 99-724-676-58691 99-724-676-58690 99-724-676-58680 99-724-676-58680 99-724-676-58680 99-724-676-58680 99-724-676-58680 99-724-676-58680 99-724-676-58680 99-724-676-58680 99-724-676-58680 99-724-676-58680 99-724-676-58680	tive trive trive trive trive trive	re 40; DB 5 d. No. 77; Mismatches
US-10-17 US-09-13 US-09-95 US-09-95 US-09-72 US-	ALIC 7246' 19/7246' 77246 37246 37246 39/72	; Sco ; Pre 3;
359 395 395 395 395 550 550 560 560 560 560 560 560 560 56	ttion US/09 triants of triants of NMBER: US/0 2022 1:sion 3.2 3:sion 3.2 44.0%; S 44.0%; S 44.0%; S 44.0%; S 151 151 2ETY 20 11 1 2ETY 20 11 1 2ETY 1501	44.0% 44.4% ative
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88888888888888888888888888888888888888	676-63963 63963, Application INFORMATION: FT COMPUGGEN LTD FERENCE: 129181.4 6APPLICATION: Varian FERENCE: 129181.4 6APPLICATION: PAPPLICATION NOIS: 972.2 6 63963 FRT BARNO SAPISION OF 563963 FRT HOMO SAPISION OF 563963 FRT HOMO SAPISION OF 563963 FRT HOMO SAPISION OF 563963 FRT SIMILARITY AAAA ABANTANESE IXACETY TWEHYXXXEES IXACETY FILL TLSEVKLEVETVIKQETY FILL COMPUGEN VALIANT COMPUGENTY FREENCE: 129181.4 FRT COMPUGEN: VALIANT COMPUGENTY FREENCE: 129181.4 FREEN	A-639 Simi 8; (
<u> </u>	ESULT 1 S-09-724-676-63963 S-09-724-676-63963 S-09-724-676-63963 GENERAL INFORMATION: APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of FILE REFERENCE: 129181.4 Compuge CURRENT FILING DAFE: 2000-11-28 NUMBER OF SEQ 1D NOS: 97222 SOFTWARR: PARENTICATION NUMBER: 05.0740-11-28 LENGTH: 2831 TYPE: PRT ORGANISM: Homo sapiens S-09-724-676-63963 QUETY MATCh Best Local Similarity 44.4%; E MATCHS 8; CONSERVATIVE 3; MATCHS 8; CONSERVATIVE 3; MATCHS 8; CONSERVATIVE 3; MATCHS 9; 1 THE REFERENCE: 129181.4 Compuge CURRENT RELING DATE: 20011-21 NUMBER OF SEQ 1D NOS: 9722 SOFTWARE: PAPELICATION NUMBER: US/ CURRENT FILING DATE: 20011-21 NUMBER OF SEQ 1D NOS: 9722 SOFTWARE: PAPELICATION NUMBER: US/ CURRENT FILING DATE: 20011-21 NUMBER OF SEQ 1D NOS: 9722 SEQ 1D NO 63963 LENGTH: 2831 TYPE: PRT	-09-724-676 Query Match Best Local Matches
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Matches 10; Conservative
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LENGTH: 1912
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                                                                                       RESULT 3

US-10-140-2

US-10-100-140-2

Sequence 2, Application US/10103140

GENERAL INFORMATION:

APPLICANT: LI, Li

APPLICANT: LI, V. Yang

TITLE OF INVENTION: Development

FILING DATE: 2002-12-30

CURRENT APPLICATION NUMBER: US 60/277,624

PRIOR FILING DATE: 2001-03-22
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Sequence 48, Application PC/TUS0221361

Sequence 48, Application PC/TUS0221361

Sequence 48, Application PC/TUS0221361

Sequence 48, Application, et al.

TITLE CURTENT: CURTENT COUTAGEN COPOCATION, et al.

FILE REFERENCE: 21402-397C

CURRENT PILLING DATE: 2001-07-03

PRIOR FILING DATE: 2001-07-03

PRIOR PELICATION NUMBER: 60/330346

PRIOR PELICATION NUMBER: 60/33038

PRIOR PELICATION NUMBER: 60/33038

PRIOR PELICATION NUMBER: 60/330380

PRIOR APPLICATION NUMBER: 60/330380

PRIOR APPLICATION NUMBER: 60/330380

PRIOR PELING DATE: 2001-09-19

PRIOR PELING DATE: 2001-07-01

PRIOR PELING DATE: 2001-07-01

PRIOR PELING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: 60/304502

PRIOR PELING DATE: 2001-07-11

PRIOR PELING DATE: 2001-07-11

PRIOR PELING DATE: 2001-07-13

PRIOR PELING DATE: 2001-07-13

PRIOR PELING DATE: 2001-07-16

PRIOR PELING DATE: 2001-07-17

PRIOR PELING DATE: 2001-07-18

PRIOR PELING DATE: 2001-07-11

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SOFTWARE: Patentin version 3.1
1484 TLSEVKLEVETVIKQETY 1501
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Best Local Similarity
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Best Local Similarity
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LENGTH: 503
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LENGTH: 1912
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Score 38; DB 1; Length 1912; Pred. No. 1.2e+02;

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APPLICANT: Anderson et al.

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-397C
CURRENT APPLICATION NUMBER: 05/303046
PRIOR PLICATION NUMBER: 60/303046
PRIOR PELICATION NUMBER: 60/303046
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2001-09-03
PRIOR FILING DATE: 2001-09-03
PRIOR FILING DATE: 2001-09-03
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-03
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-14
PRIOR FILING DATE: 2001-07-14
PRIOR FILING DATE: 2001-07-14
PRIOR PRIOR APPLICATION NUMBER: 60/305673
PRIOR FILING DATE: 2001-07-16
PRIOR PRIOR APPLICATION NUMBER: 60/305673
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/305673
PRIOR PRIOR APPLICATION NUMBER: 60/305673
PRIOR SPOTON POSE 368
NUMBER OF SEQ ID NOS: 368
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47.6%; Pred. No. 1.2e+02;
tive 2; Mismatches 3; Indels
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Sequence 52616, Application US/09724676
GENERAL INFORMATION:
FILE PEPERNCE: 129181.4 Compugen
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 52616
LENGTH: 803
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US-10-188-186-48
; Sequence 48, Application US/10188186
; GENERAL INFORMATION:
                                   Db 1463 KNT-----YEESIVGQETLR 1477
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1 KNTMEHVXXXEESIIXQETYK 21
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Best Local Similarity 47.6
Matches 10; Conservative
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; ORGANISM: Homo sapiens
US-10-188-186-48
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Best Local Similarity
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FEATURE:
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OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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   Indels
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION WUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN version 3.2
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TITLE OF INVENTION: Variants of alternative splicing
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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   Mismatches
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                                                                                                                                              US-09-724-676A-52616; Sequence 52616, Application US/09724676A; GENERAL INFORMATION:
   4;
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   Conservative
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US-09-724-676A-52616
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Matches 7; Conserv
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US-09-724-676-52629
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LENGTH: 803
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LENGTH: 986
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OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                            LOCATION: (72)..(72)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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40.7%; Score 37; DB 5; Length 986;
Best Local Similarity 35.0%; Pred. No. 93;
Matches 7; Conservative 4; Mismatches 9; Indels
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 52635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 52622, Application US/09724676
; GENERAL INFORMATION:
APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
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Pred. No. 95;
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FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 55622
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35.0%;
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                                                                                         SOFTWARE: Patentin version 3.2
SEQ ID NO 52629
LENGTH: 986
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: (61)..(61)
                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
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Best Local Similarity
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      9; Indels
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT FILION NUMBER: US/09/724,676A
CURRENT FILION DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 52622
LENGTH: 1006
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Sequence 52635, Application US/09724676A
GENERAL INFORMATION:
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 52635
LENGTH: 1006
                                                                                                                                                                                                             APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129.1914. Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 52639
LENGTH: 1006
    4; Mismatches
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                                                                 533 RNTLEKFTASIQRLIEQEEY 552
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533 RNTLEKFTASIQRLIEQEEY 552
                                       1 KNTMEHVXXXEESIIXQETY 20
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Best Local Similarity 35.09
Matches 7; Conservative
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Matches 7; Conservative
    Conservative
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; ORGANISM: Homo sapiens
US-09-724-676A-52622
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US-09-724-676A-52622
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7;
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  Matches
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                                                           Query Match

40.7%; Score 37; DB 5; Length 1006;
Best Local Similarity 35.0%; Pred. No. 95;
Matches 7; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.7%; Score 37; DB 5; Length 1006; 35.0%; Pred. No. 95; tive 4; Mismatches 9; Indels
                                                                                                          9; Indels
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181-4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 52639
LENGTH: 1006
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                                                                                                                                                                                                                                                                                               ; Sequence 52639, Application US/09724676A; GENERAL INFORMATION:
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533 RNTLEKFTASIQRLIEQEEY 552
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Best Local Similarity 35.0*
; ORGANISM: Homo sapiens
US-09-724-676A-52635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-52639
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US-09-724-676A-52639
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments)
109.706 Million cell updates/sec February 11, 2003, 18:14:11; Search time 18.4021 Seconds Run on:

1 KNTMEHVXXXEESIIXQETYK 21 US-09-380-738A-4 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	alpha-s2-casein pr	alpha s2-casein -	alpha-s2-casein pr	alpha-s2-casein pr		bacillolysin (EC 3		aspartate dehydrog	deh	hypothetical prote	probable cell cycl		site-specific DNA-	hypothetical prote	protein T16E15.12		thetical p			division	⊆	pothetical		ď		뒽	s S	14	chromosomal protei
		ID	KABOS2	A48383	KASHS2	JN0547	I46995	HYBSU	F83804	E86621	G72002	T51995	T39266	G71611	141076	T23904	D86355	E86355	T25536	A45278	680639	AF0517	G85490	F86191	W2WL33	T21188	S22027	T48318		88	T46486
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ф		Match	95.6	S	59.9	ω	8	9	44.0	43.4	43.4	42.9		42.9		41.8		41.8	41.2	40.7	40.7	40.7	40.7	40.7	40.7	40.7	40.7	40.7	40.7	40.7	40.7
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hypothetical prote	hypothetical prote	acetyltransferase	LysR-family transc	hypothetical prote	choline kinase - h	L-serine dehydrata	hypothetical prote	hypothetical prote	VPS27 protein - ye	transcription regu	conserved hypothet	cell division prot	glycosyl transfera	BNI4 protein - yea	genome polyprotein
T00167	A70168	H82684	AB0312	T43750	S23104	D82974	T05136	D82902	S45129	D95249	A98114	A70132	A95206	863199	RRXPLC
2	~	7	~	~	7	7	~	7	7	7	7	7	N	7	7
91	286	305	310	447	456	458	577	578	622	979	949	787	814	892	2210
39.6	39.6	39.6	39.6	39.6	39.6	39.6	39.6	39.6	39.6	39.6	39.6	39.6	39.6	39.6	39.6
36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36
30	31	32	33	34	35	36	37	38	39	40	41	42	4.3	44	45

ALIGNMENTS

Н	
ULT	SS
RES	KAB

A;Status: translation not shown A;Status: translation not shown A;Status: translation A;Status: 1-222 cGND-A;Cross-references: GB:M94327 R;Stewart, A.F.; Bonsing, J.; Beattie, C.W.; Shah, F.; Willis, I.M.; Mackinlay, A.(MOL. Biol. Evol. 4, 231-241, 1987 MAI: Evol. 4, 231-241, 1987 A;Fitle: Complete nuclectide sequences of bovine alpha-s2- and beta-casein cDNAs: A;Reference number: A93062; MUID:88188989; PMID:2833669

A;Status: translation not shown A;Molecule type: mRNA A;Residues: 1-222 <STE> A; Accession: A29087

A;Cross-references: GB:M16644; NID:g162928; PIDN:AAA30479.1; PID:g162929 A;Cross-references: DB:M16644; NID:g162928; PIDN:AAA30479.1; PID:g162929 R;Brignon, G.; Ribadeau Dumas, B.; Mercier, J.C.; Pelissier, J.P.; Das, B.C. FEBS Lett. 76, 274-279, 1977

A; Title: Complete amino acid sequence of bovine alpha-S2-casein. A; Reference number: A91438; MUID:77185633; PMID:862906 A; Contents: A allele

A; Accession: A91438

A;Molecule type: protein A;Residues: 16-101, 'EE', 104-222 <BRI> A;Note: four fractions, previously designated s2, s3, s4, and s6, appear to have

R,Grosclaude, F.; Joudrier, P.; Mahe, M.F. J. Dairy Res. 46, 211-213, 1979

A; Title: A genetic and biochemical analysis of a polymorphism of bovine alpha-s2-c A; Title: A genetic and biochemical analysis of a polymorphism of bovine alpha-s2-c A; Reference number: A92771; WuID: 79239837; PMID:469044
A; Contents: annotation; D allele
A; Note: the sequence of the D allele has a deletion of nine residues, which may be R; Zuccht, H.D.; Raida, M.; Adermann, K.; Maegert, H.J.; Forssmann, W.G.
R; Research and A; 185-188, 1995
A; Title: Casocidin-I: a casein-alpha(s2) derived peptide exhibits antibacterial ac A; Reference number: S66626; MUID:96000204; PMID:7556666

A,Accession: S66626
A,Molecule type: protein
A,Residues: 165-203 <2UC>
C,Comment: The sequence of the A allele is shown.
C,Genetics:

A; Gene: alphas2ca

A; Map position: 6 A; Introns: 17/3; 26/3; 33/3; 47/3; 56/3; 65/3; 74/3; 82/3; 97/3; 138/3; 147/3; 156

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Query Match 59.99
Best Local Similarity 59.13
Matches 13; Conservative
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession. 425070; S17866
R;Boisnard, M.; Petrissant, G.
Biochimle 67, 1043-1051, 1985
A;Title: Complete sequence of ovine alpha-s2-casein messenger RNA.
A;Reference number: A25070; MUID:86104467; PMID:3002499
A;Accession: A25070
A;Molecule type: mRNA
A;Residues: 1-223 < BOI>
A;Cross-references: GB:X03238; NID:91238; PIDN:CAA26983.1; PID:9732894
A;Cross-references: GB:X03238; NID:91238; PIDN:CAA26983.1; PID:9732894
B;Boisnard, M.; Hue, D.; Bouniol, C.; Mercier, J.C.; Gaye, P.
Bur. J. Biochem. 201, 633-641, 1991
A;Title: Multiple mRNA species code for two non-allelic forms of ovine alphas2-casein.
A;Reference number: S17856; MUID:92037619; PMID:1935959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F.1-15/Domain: signal sequence #status predicted <SIG>
F.16-223/Product: alpha-s2-casein #status predicted <KA2>
F.23.24,25,72,73,74,77,145,147,159/Binding site: phosphate (Ser) (covalent) #status F;53,88,146,154,170,198/Binding site: phosphate (Thr) (covalent) #status
                    C;Keywords: mammary gland; milk; phosphoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-222/Product: alpha-s2-casein #status experimental <MAT>
F;23,24,25,31,71,72,73,76,144,146,158/Binding site: phosphate (Ser) (covalent) #status
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha s2-casein - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 03-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary
A:Status: preliminary
A:Status: preliminary
A:Residues: 1-235 AALE>
A:Reperimental source: mammary gland
A:Reperimental source: mammary gland
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:110884, NCBIP:110885)
C;Superfamily: alpha-s2-casein
                                                                                                                                                                                                                                       Gaps
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Pred. No. 0.0011;
1; Mismatches 6; Indels
                                                                                                                                                                            Length 222
                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: A48883
R;Alexander, L.J.; Das Gupta, N.A.; Beattie, C.W.
Anim. Genet. 23, 365-367, 1992
A;Title: The sequence of porcine alpha s2-casein cDNA.
A;Reference number: A48383; MUID:92367960; PMID:1503276
A;Accession: A48383
                                                                                                                                                                       95.6%; Score 87; DB 1; I
81.0%; Pred. No. 5.5e-09;
live 0; Mismatches 4;
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A Molecule type: mRNA
A Molecule 193, T', 95-223 <B02>
C; Superfamily: alpha-s2-casein
C; Keywords: mammary gland; milk; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 KHEMEHVSSSEESINISQEKYK 37
                                                                                                                                                                                                                                                                                                             16 KNTMEHVSSSEESIISQETYK 36
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                                                                                                                                                                                                                                                                                1 KNTMEHVXXXEESIIXQETYK 21
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C; Superfamily: alpha-s2-casein
                                                                                                                                                                                                                              Conservative
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Les 17; Conserv
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                                                                                                                                                                       Query Match
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C. Species: Capra aggagus hircus (domestic goat)

C. Species: Capra aggagus hircus (domestic goat)

C. Species: Capra aggagus hircus (domestic goat)

C. Saccession: S33881. S33880, JuN547, 220620

C. Accession: S33881. S33880

A. Title: Characterization of G.; Mahe, M. F.; Printz, C.

Protein Seq. Data Anal: 5, 213-218, 1993

A. Title: Characterization of G. Anal: 5, 213-218, 1993

A. Molecule type: protein

A. Molecule type: mRNA

A. Reference number: JNO547; MUID: 93216130; PMID: 9462880

A. Molecule type: mRNA

A. Residues: 1-78, E. Mos-223 < Bos-223 <
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A; Title: Biochemical and genetic analysis of variant C of caprine alpha s2-casein (CA); Reference number: 146995; MUID:95030556; PMID:7943951
                                                                                               1;
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C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 13-Aug-1999
C;Accession: I46995
R;Bouniol, C.;_Brignon, G.; Mahe, M.F.; Printz, C.
                                                                                               Gaps
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                                                                                       1;
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Score 54.5; DB 1; Length 223; Pred. No. 0.009; 1; Mismatches 7; Indels
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                                                                                  1;
                                                                                                                                                                                                           16 KHKMEHVSSSEEPINISQEIYK 37
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    59.9%;
59.1%;
                                                                                                                                                             1 KNTMEHVXXXEESI-IXQETYK
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Best Local Similarity
Matches 13; Conserv
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7; Indels

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A; Cross-references: GB: AP001511; GB: BA000004; NID: 910173727; PIDN: BAB04957.1; GSPD
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A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: G72002
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A;Experimental source: strain CWL029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aspartate dehydrogenase [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: E86621
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:BA000008; NID:g8979421; PIDN:BAA99255.1; GSPDB:GN00142
A;Experimental source: strain J138
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: G72002
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                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 2; Length 300;
Pred. No. 7.5;
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                                                                                                                                                                                  A)Experimental source: strain C-125
C,Genetics:
A,Gene: BH1238
C,Superfamily: conserved hypothetical protein MJ0449
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45.0%; Pred. No. 10;
tive 4; Mismatches
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Best Local Similarity
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A; Residues: 1-333 <ARN>
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Matches 7; Conserv
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A; Residues: 1-333 <STO>
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                                       A; Status: preliminary
A; Molecule type: DNA
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A; Accession: F83804
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R,Sidler, W.; Niederer, E.; Suter, F.; Zuber, H.
Biol. Chem. Hoppe-Seyler 367, 643-657, 1986
A,Title: The primary structure of Bacillus cereus neutral proteinase and comparison with A,Reference number: A2306, MUID:87000170; PMID:3092843
A,Reference number: A24306
A,Molecule type: protein
A,Residues: 250-566 < SID>
A,Resperimental source: strain DSM3101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Crystal structure of neutral protease from Bacillus cereus refined at 3.0 A res
A;Reference number: A38850; MUID:88172498; PMID:3127592
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Bacillus cereus
C; Species: Bacillus cereus
C; Date: 30-Jun-1988 #sequence_revision 12-Apr-1996 #text_change 15-Sep-2000
C; Date: 30-Jun-1988 #sequence_revision 12-Apr-1996 #text_change 15-Sep-2000
C; Accession: S22690; A24306; 139914
R; Wetmore, D.R.; Wong, S.L.; Roche, R.S.
Mol. Microbiol. 6, 1593-1604, 1992
Mol. Microbiol. 6, 1593-1604, 1992
A; Title: The role of the pro-sequence in the processing and secretion of the thermolysin A; Reference number: S22690; MUID:92356823; PMID:1495388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 250-566
R; Pauptit, R.A.; Karlsson, R.; Picot, D.; Jenkins, J.A.; Niklaus-Reimer, A.S.; Jansonius J. Mol. Biol. 199, 525-537, 1988
                                                                                                                                                                                                                                                                                                                                  bacillolysin (EC 3.4.24.28) precursor [validated] - Bacillus cereus
N;Alternate names: Bacillus metalloendopeptidase; microbial metalloproteinase; neutral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Stark, W.; Pauptit, R.A.; Jansonius, J.N.
submitted to the Brookhaven Protein Data Bank, January 1992
A;Reference number: A51318; PDB:1NPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 6.3;
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                                                                                           16 KHKMEHVSSSEEPINIFQEIYK 37
                                                    1 KNTMEHVXXXEESI-IXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 NTIDHVTNDDKSPVKQEAPK 240
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A; Residues: 1-566 <WET>
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A;Gene: cnp; nprC
C;Function:
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DB 2; Length 333;

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C; Specias: BSCHEALURA COLL
C; Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 04-Mar-2000
C; Accession: S53984; I41076
K; Lee, K.E.; Kam, K.M., Shaw, P.C.
Nucleic Acids Res. 23, 103-108, 1995
A; Title: A bacterial methyltransferase M.EcoHK311 requires two proteins for in vitr A; Recession: S53984
A; Accession: S53984
A; Molecule type: DNA
A; Restances: EMBL: X82231; NID:95175351; PMID:9639973
A; Restances: EMBL: X82231; NID:9639971; PID:9639973
A; Restances: EMBL: X82231; NID:9639971; PID:9639973
A; Note: the authors translated the codon TTG for residue 97 as Met
A; Note: part of this sequence, including the amino end was confirmed by protein seq
C; Complex: heterodimer; beta chain is encoded by an alternative reading frame with:
C; Superfamily: Escherichia coli site-specific DNA-methyltransferase (cytosine-specific Skeywords: heterodimer; methyltransferase; restriction modification system; S-aden.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) EcoHK31I beta
                                                                   A;Cross-references: GB:AE001403; GB:AE001362; NID:g3845216; PIDN:AAC71901.1; PID:g:
A;Experimental source: clone 3D7
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C;Species: Caenorhabditis elegans
C;Decies: Caenorhabditis elegans
C;Decies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T23904
R;Swinburne, J.
R;Swinburne, J.
R;Swinburne, J.
R;Reference number: 219815
A;Accession: T23904
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                                                                                                                                                                                                                                                                                         Length 2206;
                                                                                                                                                                                                                                        42.9%; Score 39; DB 2; Length 2zu-
36.8%; Pred. No. 1.1e+02;
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ed. No. 19;
Mismatches 8
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41.2%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           726 NDMYHIHNDENDVINOKLY 744
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Best Local Similarity 30.00
Best Local 7; Conservative
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Matches 7; Conservative
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Best Local Similarity
                               A; Residues: 1-2206 <GAR>
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                                                                                                                                                   C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: 20S cyclosome complex formation and proteolytic activity inhibited by the cAMP/
A; Reference number: 225896
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R.Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M.
Submitted to the EMBL Data Library, August 1999
A; Reference number: 221840
A; Accession: T39266
A; Accession: T39266
A; Accession: T39266
A; Stepliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1458 < LIN>
A; Cross references: EMBL:AL110295; PIDN:CAB53725.1; GSPDB:GN00067; SPDB:SPBC106.09
A; Edenetics: Strain 972h-; cosmid c106
C; Genetics: A; Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                 H.; Yanagida, M.
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                                                                                                                                                                                                                                                                                     C. Species: Schizosaccharomyces pombe
C. Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
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Nature 384, 276-279, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1458;
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68;
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68;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-1458 <YAM>
A; Cess-references: EMBL:D85196; PIDN:BAA22618.1
C; Genetics:
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42.1%; Pred. No. 68;
Live 2; Mismatches
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42.1%; Pred. No.
939 TMEEILASNESELKNEGYK 957
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Best Local Similarity 42.18
Matches 8; Conservative
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Matches 8; Conserv
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Best Local Similarity 50.v.
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70 KKSMEHVYALEEKL 83
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A; Residues: 1-871 <STO>
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A; Map position: 1
RESULT 15
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Search completed: February 11, 2003, 18:21:17 Job time: 19.4021 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 11, 2003, 18:07:35 ; Search time 9.30928 Seconds (without alignments) 93.563 Million cell updates/sec Run on:

1 KNTMEHVXXXEESIIXQETYK 21 US-09-380-738A-4 91 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

112892 seqs, 41476328 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		đ			SOMETHE	
Result		Query				,
No.	Score	Match	Length	DB	OI	Description
1	87	92.6	222	Н	CAS2_BOVIN	pos
7		65.4	235	Н	CAS2_PIG	39036 sus
e		59.9	223	~	CAS2_SHEEP	04654
4	53.5	8	223	Н	CAS2_CAPHI	-
S	42	9	566	,	NPRE_BACCE	9
9	39	α.	1458	Н	CUT4_SCHPO	C)
7	37	0	121	П	FTSL_ECOLI	18
· oc	37	40.7	353	-	VE2_HPV33	
0	37	0	477	Н	MY SO_DROME	
10	37	40.7	875	Н	TP3B_DROME	_
11	37	40.7	879	Н	MYSP_DROME	
12	36	39.6	456	, ,	KICH_HUMAN	0
13	36		622	Н	VP27_YEAST	m
14	36	39.6			SPOT_SPICI	~
15	36	39.6		Н	RELA_MYXXA	
16	36	39.6		Н	BNI4_YEAST	m
17	36	39.6		Н	RRPO_LYCVA	
18	35.5	39.0		Н	MP44_SFVKA	Q9q926 shope fibro
19	35	38.5		~	FUMA_METJA	Q58690 methanococc
20	35	38.5		Н	ELL2_HUMAN	
21	35	38.5		Н	YCCS_HAEIN	9 7
22	35	38.5		Н	YK76_YEAST	~
23		37.9	223	Н	CAS2_CAVPO	
	34.5	37.9		٦	MP44_MYXVL	Q9q8q1 myxoma viru
	34	37.4		7	YPB3_LACLA	
26	34	37.4		-	ISTB_PSEAE	
27	34	37.4		Н	YF09_MYCTU	œ
28	34	37.4		7	TRPG_PICAN	o o
29	34	37.4		7	THD1_LACLA	2
30	34	37.4		Н	CLPX_AZOVI	m
31	34	37.4	8	Н	TRPG_YEAST	_
32	34	37.4	528	Н	WR42_ARATH	
33	34	37.4	9	Н	X397_MYCPN	Q50333 mycoplasma

P34909 saccharomyc	050581 staphylococ	Q10039 caenorhabdi	P47582 mycoplasma	Q9hau6 homo sapien	097944 camelus dro	P27089 gallus gall	Q00179 aspergillus	Q9v116 pyrococcus	074019 pyrococcus	PO2014 taricha gra
NOT4_YEAST	RECG STAAU	SYG_CAEEL	RPOC_MYCGE	FKG2_HUMAN	CAS2_CAMDR	XPA_CHICK	SR54_ASPNG	RPOH_PYRAB	RPOH_PYRHO	HBA_TARGR
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587	612 686	742	1292	173	193	267	534	82	82	142
37.4	37.4	37.4	37.4	36.8	36.8	36.8	36.8	36.3	36,3	36.3
34	34 34	34	34	33.5	33.5	33.5	33.5	33	33	33
34	32	37	38	36	40	41	42	43	44	45

ALIGNMENTS

IN SEOVIN STANDARD; PRT; 222 AA.	PU2063; Q9TR51; 21-JUL-1986 (Rel. 01, Created) 01-JUL-1989 (Rel. 11, Last sequence update) 15-JNN-2002 (Rel. 41, Last annotation update)	Alpha-S2 casein precursor [Contains: Casocidin-I]. CSNIS2.	Bos taurus (Bovine). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	malia; Eutheria; Cetartiodactyla; Kuminantia; Fectia; Dovoluca; idae; Boyinae; Bos.	NCBI_TaxID=9413;	4ed=2833669;	Stewart A.F., Bonsing J., Beattle C.W., Shan F., Wills I.M., Mackinlav A.G.:	"Complete nucleotide sequences of bovine alpha S2- and beta-casein	Biol. Evol. 4:231-241(1987).	12] SEQUENCE OF 16-222 (A ALLELE).	TISSUE=Milk; MEDLINE=77185633; PubMed=862906;	Brignon G., Ribadeau-Dumas B., Mercler JC., Pelissier JP.,	Das B.C.; "Complete amino acid sequence of bovine alphaS2-casein.";	(1977).	[3] PARTIAL SEQUENCE (D ALLELE).	TISSUE=Milk;		"A genetic and biochemical analysis of a polymorphism of bovine alpha	S2-casein."; J. Dairy Res. 46:211-213(1979).	SEQUENCE OF 165-203, AND CHARACTERIZATION OF CASOCIDIN. TTSSUE=Milk:	0204; PubMed=7556666;	Zucht HD., Raida M., Adermann K., Meagert Hט., Folssmann איישיי "ראבסטולוחידי א ראבאווי-אומוא S. derived peptide exhibits antibacterial	casciulty.";	FEBS Lett. 372:185-188(1995). FINCTION: IMPORTANT ROLE IN THE CAPACITY OF MILK TO TRANSPORT		 FUNCTION; CASOCIDIN-I INHIBITS THE GROWTH OF ESCHEMICHIA COLI AND STAPHYTOCOCCUS CARNOSUS. 	SUBCELLULAR LOCATION: Extrac	 TISSUE SPECIFICITY: MAMMARY GLAND; MILK. MASC SERVINGMETRY: MW=4870: MFTHOD=Electrospray; RANGE=165-203. 	POLYMORPHISM: AT LEAST TWO ALLELES EXIST. THE SEQUENCE OF THE	ALLELE IS SHOWN HERE. THE D ALLELE SEQUENCE DIFFERS FROM 1781 SHOWN IN HAVING A DELETION OF NINE RESIDUES, WHICH MAY BE 49-58,	
SUL S2_	AC PUZE DT 21-0 DT 01-1						RA Ster				RC TIS		RA Das		RN [3] RP PAR		RX MED RA Gro			RP SEQ		RA Zuc		RL FEB		55 -!-	-	7 7	-i-	SSS	
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                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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           SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
DATABASE: NAME-Protein Spotlight;
NOTE-Issue 16 of November 2001;
WWW-"http://www.expasy.org/spotlight/articles/sptlt016.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alexander L.J., Das Gipta N.A., Beattie C.W.;
"The sequence of porcine alpha s2-casein cDNA.";
Anim. Genet. 23:365-367(1992).
-!- FUNCTION: IMPORTANT ROLE IN THE CAPACITY OF MILK TO TRANSPORT
CALCIUM PHOSPHATE.
-!- SUBCELLULAR LOCATION: Extracellular.
-! TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-!- TISSUE SPECIFICITY: MAMMARY GLAND;
-!- SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.6%; Score 87; DB 1; Length 222; 81.0%; Pred. No. 4.9e-09; ive 0; Mismatches 4; Indels
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81E7408AF1C12F7C CRC64;
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                          PIK; AZYOUK; AZYOUK,
INTERPRO; IPRO01588; Casein.
Prom; Pr00363; caseins; 2.
PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Mammary gland;
MEDLINE=92367960; PubMed=1503276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KNTMEHVXXXEESIIXQETYK 21
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PIR; A29087; A29087.
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17;
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P39036;
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CONFLICT
SEQUENCE
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MOD_RES
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Biochimie 67:1043-1051(1985).
-!- FUNCTION: IMPORTANT ROLE IN THE CAPACITY OF MILK TO TRANSPORT
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-!- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-!- SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
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Pred. No. 0.00069;
; Mismatches 6;
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13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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ALPHA-S2 CASEIN
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Boisnard M., Petrissant G.;
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63.6%;
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InterPro; IPR001588; Casein.
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NCBI_TaxID=9940;
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P04654;
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CAS2_SHEEP
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
POLYMORPHISM: THREE ALLELES OF ALPHA-S2 CASEIN ARE KNOWN: A, B AND
C. THE FREQUENCIES OF THE ALLELES IS ESTIMATED TO BE 0.85, 0.04
AND 0.11 IN THE FRENCH DALRY BREEDS 'ALPINE' AND 'SAANEN'.
SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDILINE-95030556; PubMed=794951;
Bouniol C., Brignon G., Mahe M.F., Printz C.;
"Biochemical and genetic analysis of variant C of caprine alpha s2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capra hircus (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
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Anim. Genet. 25:173-177(1994).
-!- FUNCTION: IMPORTANT ROLE IN THE CAPACITY OF MILK TO TRANSPORT
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Pred. No. 0.0056;
1; Mismatches 7; Indels
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; 67212935E27426D7 CRC64;
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16-OCT-2001 (Rel. 40, Last annotation update)
Alpha-S2 casein precursor (Alpha-S2-CN).
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                        PS00306; CASEIN_ALPHA_BETA; 1.
                                                 Milk; Phosphorylation; Repeat; Signal.
SIGNAL 1 15
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26332 MW;
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nilarity 59.1%;
Conservative 1
Pfam; PF00363; caseins; 2
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P33049;
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MEDLINE=92356823; PubMed-1495388;
Wetmore D.R., Wong S.L., Roche R.S.;
"The role of the pro-sequence in the processing and secretion of the thermolysin-like neutral protease from Bacillus cereus.";
Mol. Microbiol. 6:1593-1604(1992).
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Pauptit R.A., Karlsson R., Picot D., Jenkins J.A.,
Niklaus-Reimer A.-S., Jansonius J.N.;
Niklaus-Reimer A.-S., Jansonius J.N.;
"Crystal structure of neutral protease from Bacillus cereus refined at 3.0-A resolution and comparison with the homologous but more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sidler W., Niederer E., Suter F., Zuber H.;
"The primary structure of Bacillus cereus neutral proteinase and comparison with thermolysin and Bacillus subtilis neutral proteinase.";
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SIMILARITY)
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SIMILARITY)
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16-OCT-2001 (Rel. 40, Last annotation update)
Bacillolysin precursor (EC 3.4.24.28) (Neutral protease).
NPR. OR NPRC.
                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1396;
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                                                                                                           Interrus, L. V. Caseins; 2. Priam; PF00363; caseins; 2. Prossire; PS00306; CASEIN, ALPHA_BETA; 1. Milk; Phosphorylation; Signal; Repeat; Polymorphism. BY SIMILARITY.
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or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
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MEDLINE=87000170; PubMed=3092843;
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                        EMBL; X65160; CAA46278.1; -.
EMBL; S74171; AAB32166.1; -.
PIR; S20620; S20620.
PIR; JN0547; JN0547.
PIR; S33880; S33880.
PIR; S33881; S33881.
                                                                                                                                                                                                                                                                                                                                                         26389 MW;
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59.1%;
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Matches 13; Conservative
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                                MEDLINE-92339470; PubMed-1633827; Zark W., Pauptit R.A., Wilson K.S., Jansonius J.N.; "The structure of neutral protease from Bacillus cereus at 0.2-nm resolution.";
                                                                                  InterPro; IPR005075; Pep_M4_propep.
InterPro; IPR005070; Peptidase_M4.
InterPro; IPR00130; Zn_WTpeptdse.
InterPro; IPR00130; Zn_WTpeptdse.
InterPro; IPR00130; Zn_WTpeptdse.
Pfam; PF02468; Peptidase_M4_C; 1.
Pfam; PF03413; Pep_M4_propep; 1.
PRNNTS; PR00730; THERMOLYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Calcium; Zinc; 3D-structure; Signal.
                                                                                                                                                        -1- COFACTOR: BINDS 1 ZINC ION. BINDS FOUR CALCIUM IONS (BY SIMILARITY).
                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M4.
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ZINC (CATALYTIC).
PROTON DONOR.
                                                                                                                                                                                                                                                                                                                                                                                                               BACILLOLYSIN
                        K-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                   Eur. J. Biochem. 207:781-791(1992).
thermostable enzyme thermolysin.";
J. Mol. Biol. 199:525-537(1988).
                                                                                                                                                                                                                                                                    EMBL; M83910; AAA22620.1; -. PIR; A24306; HYBSU. PDB; INPC; 31-OCT-93. PDB; ISPB; O7-DEC-95. MEROPS; M04.015; -.
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Mod V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Mod V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Mod V., Gwilliam R., Bayles J., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Havis P., Feltwell T., Fraser A.,
Holroyd S., Hornsby T., Howarth S., Hudtle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungail K., Murphy L., Niblett D., Odell C.,
Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Modward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schapet E., Moestl D., Hilbert H.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complex formation and proteolytic activity inhibited by
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND FUNCTION.
MEDLINE=9707875; PubMed=8918880;
Yamashita Y.M., Nakaseko Y., Samejima I., Kumada K., Yamada H.,
Michaelson D., Yanaqida M.;
                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                 Length 566;
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                                                                                                                                                                                                                                                        60919 MW; E18B4572C2C4E1D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                              46.2%; Score 42; DB 1;
40.0%; Pred. No. 3.2;
tive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     CUT4_SCHPO STANDARD; PRT; 1458 AA. 09URV2; 013457; 16-07-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                221 NTIDHVTNDDKSPVKQEAPK 240
                                                                                                                                                                                                                                                                                                                                   NTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the CAMP/PKA pathway.";
Nature 384:276-279(1996).
                                                                                                                                                                                                                                                                                                          8; Conservative
                                   Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cut4 protein.
CUT4 OR SPBC106.09.
                                                                                                                                                                                                                                                        566 AA;
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Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hurt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., The genome sequence of Schizosaccharomyces pombe.", "The genome sequence of Schizosaccharomyces pombe.",
                                                                                                                                                                                          -i- FUNCTION: Has an essential role in the regulation of 20S cyclosome complex formation. Mutations to this protein prevent the exit from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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MEDLINE=9307472; PubMed=1447153;
UGKI M., Wachi M., Jung H.K., Ishino F., Matsuhashi M.;
"Escherichia coli mraR qene involved in cell growth and division.";
J. Bacteriol. 174:7841-7843(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93077455; PubMed=1332942; Guzman L. M., Barondess J.J., Beckwith J.; Fists, an essential cytoplasmic membrane protein involved in cell division in Escherichia coli."; J. Bacteriol. 174:7716-7728(1992).
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Pred. No. 31; 
2; Mismatches 9; Indels
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1458 AA; 165409 MW; 182E65BDA3A82183 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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FTSL OR MRAR OR B0083 OR Z0093 OR ECS0087.
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MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genomic sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.";
Nucleic Acida Res. 18:2813-2813(1990).
-!- FUNCTION: PROTEIN INVOLVED IN CELL DIVISION AND CELL GROWTH. MAY
PLAY SOME ROLE IN COUPLING CELL DIVISION AND PEPTIDOGLYCAN
                                                                                                                                                       Nakamura M., Maruyama I.N., Soma M., Kato J., Suzuki H., Horota Y.; "On the process of cellular division in Escherichia coli: nucleotide sequence of the gene for penicillin-binding protein 3."; Mol. Gen. Genet. 191:1-9(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-0157:H17 / BDL933 / ATCC 700927;
STRAIN-0157:H17 / BDL933 / ATCC 700927;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpetrick H.A.,
Rose D.J., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anautharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gomez M.J., Fluoret B., van Heijenoort J., Ayala J.A.; "Nucleotide sequence of the regulatory region of the gene pbpB of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell division; Transmembrane; Inner membrane; Complete proteome.
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Pred. No.
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MEDLINE=90251464; Pubmed=2187182;
                                                                                                    STRAIN=K12;
MEDLINE=83296957; PubMed=6350821;
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EMBL; S49802; AAB24311.1; -.
EMBL; X55034; CAA38860.1; -.
EMBL; AE000118; ARC73194.1; -.
EMBL; K00137; AAA24299.1; -.
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                                                                 PRELIMINARY SEQUENCE FROM N.A.
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Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:529-533(2001).
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PIR; A45278; A45278
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Best Local Similarity

"The complete genome sequence of Escherichia coli K-12.";

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                                                                                                                                                                                                                                                                            Cole S.T., Streeck R.E.,
"Genome organization and nucleotide sequence of human papillomavirus
"Genome organization and nucleotide sequence of human papillomavirus
"Genome organization and nucleotide sequence of human papillomavirus
"Genome organization and nucleotide sequence of human papillomavirus
Type 33, which is associated with cervical cancer.";
J. Virol. 58:991-995 (1986)
J. PREDIATION SET REPORTS VIRAL TRANSCRIPTION AND DNA REPLICATION.
IT BINDS TO THE EZER RESOLATORY REGION. IT CAN EITHER
ACTIVATE OF REPRESS TRANSCRIPTION DEPRNDING OF EZRE'S POSITION
WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
BY STERICALLY HINDERING THE ASSENBLY OF THE TRANSCRIPTION
INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R PIR; A0367U; m.c...

R PIR; A0367U; m.c...

R HSSP; P17383; 1DHM.

DR InterPro; IPR000427; E2_C.

DR InterPro; IPR000466; E2_N.

DR Pfam; PF00511; E2_C; 1.

DR ProDom; PD000678; E2_L; 1.

DR ProDom; PD000678; E2_L; 1.

DR Proton; PT000678; E2_L; 1.

RW Early protein; Transcription regulation; Activator; DNA-binding; m.ans-acting factor; DNA replication; Repressor; Nuclear protein.

""" AA; 40253 MW; 673A9D765DBB11BC CRC64;

""" AA; A0253 MW; 673A9D765DBB11BC CRC64;
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
     .
0
     Indels
                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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9
                                                                                                                                              01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                            353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  477 AA.
 5; Mismatches
                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: BINDS DNA AS A DIMER.
                                                                                                                                                                                                                                                                      MEDLINE=86200464; PubMed=3009902;
                                                                                                                                 01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYSQ_DROME STANDARD;
P35416; Q9VSP5;
01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                              Human papillomavirus type 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M12732; AAA46961.1; -. PIR; A03670; W2WL33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 KNTMDYTNWGEIYIIEEDT 144
                                       104 KLQMQHVDPSQENIVVQK 121
                       1 KNTMEHVXXXEESIIXQE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KNTMEHVXXXEESIIXQET 19
7; Conservative
                                                                                                           STANDARD;
                                                                                                                                                                       Regulatory protein E2.
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  NCBI_TaxID=10586;
                                                                                                                                                                                                                                                                                                                                                                                                                   REPLICATION.
                                                                                                                                                                                                                     Papillomavirus
                                                                                                        VE2_HPV33
P06423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYSQ_DROME
Matches
                                                                                               VE2_HPV33
                                                                                   RESULT 8
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16-027-2010 (Rel. 20, Last entendence update)

16-027-2010 (Rel. 20, Last entendence update)

18-027-2010 (Rel. 20, March 19, March 19, March 19, Relation of a movel isoform unscennerable perapotal perapotal update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update update
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Adams M.D., Celliker S.E., Holf R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Gocage R.A., Lewisz S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandaell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D., Na M. K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikkos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Buck J., Broatler F., Center A., Chandra I., Borkova D., Botchan M.R., Buck G., Davenport L.B., Davies P., Ab Dodson K., Doup L.E., Downes M., Dugan-Roche S., Dunkov B.C., Dunk D., Dav D., Dow I., Dietz S.M., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., An Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                     Coiled coil; Muscle protein; Thick filament; Myosin; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson T.M., Chen A.D., Hsieh T.-S.; "Cloning and characterization of Drosophila topoisomerase IIIbeta. Relaxation of hypernegatively supercoiled DNA."; J. Biol. Chem. 275:1533-1540(2000).
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                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL).
NONHELICAL REGION (POTENTIAL).
3FD4876F12EB0828 CRC64;
                                                                                                                                                                                                                                                                         NONHELICAL REGION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 1; Length 477;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., FUNCTION, AND DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TP93B_DROME STANDARD; PRT; 875 AA. 096551, 09W416; 51, 09W416; 61, 09W42000 (Rel. 39, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) DNA topoisomerase III beta (EC 5.99.1.2). TOP3 -BETA OR TOP3 OR CG3458.
                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IISSUE=Embryo;
MEDLINE=20102653; PubMed=10636841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20196006; PubMed=10731132;
                                                                                                                                EMBL; AE003554; AAF50371.1;
PIR; S22027; S22027.
PIR; S2P037; PIR.
InterPro; IPR002928; Myosin_tail.
Pfam; PF01576; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                 54889 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 KHVVEQVHEEQERIVKLETIK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KNTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                       40.7%;
                                                                                                                    EMBL; X62591; CAA44476.1;
                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 38.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                             456
                                                                                                                                                                                                                                                         Alternative splicing
                                                                                                                                                                                                                                                                                                                             477 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Berkeley;
                                                                                                                                                                                                                                                                               1
108
457
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Lu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.

RA Mattov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Melson D.R., Nelson K.A., Nixon K., Muskern D.R., Pelceb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Ra Shue B.C., Siden-Klanos II., Simpson M., Strong R., Sun E.,

Soler E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Soler E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Soler E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Soler E., Laveri J.S., Lan M., Weissenbach J.,

Milliams S.M., Woodage T., Worley K.C., Wun D., Yang S., Yao Q.A.,

RA Then S.M., Myers E.W., Rubin G.M., Venter J.C.;

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT Grence 287:2185-2195(200).

C.I. CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded

C. I. CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded

C. I. CATALYTIC ACTIVITY: LEVELS DECLINE DIRING LARVAL AND PUPAL

C. STAGES RAMENTAL STAGE: EXPRESSED DURING THE FIRST 6 HOURS OF

EMBRYONIC DEVELOPMENT, LEVELS DECLINE DIRING LARVAL AND PUPAL

C. STAGES RAMENTAL STAGE: EXPRESSED DURING THE FIRST 6 HOURS OF

C. STAGES RAMENTAL STAGE: EXPRESSED DURING THE FIRST 6 HOURS OF

C. STAGES RAMENTAL STAGE: EXPRESSED DURING THE FIRST 6 HOURS OF

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND (BY SIMILARITY). SHILLARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA CLEÁVAGE (BY SIMILARITY).
GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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3A26520C10AB6057 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00396; TOPOISOMERASE_I_PROK; 1.
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InterPro; IPR002956; DNAprim_toprim.
InterPro; IPR003601; DNAtop1_DNA_bind.
InterPro; IPR003602; DNAtop1_DNA_bind.
InterPro; IPR000380; Prok_tpisomrase.
Pfam; PF01131; Topoisom_bac; 1.
SPART; SM00437; ToPIAc; 1.
SMART; SM00436; TOPIBc; 1.
SMART; SM00436; TOPIBc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isomerase; Topoisomerase; DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003437
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MYSP_DROME
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REALINE-SCIURINGE FOR NA.

REALINE-SCURINGE FOR NA.

REALINE-SCURINGE FOR SCHOLAGE 10731132;

RA Adams M.D., Celniker S.E., Holt E.M., Hoskins R.A., Galle R.F.,
Adams M.D., Celniker S.E., Holt E.M., Ashburner M., Hienderson S.N.,
RA Adams M.D., Celniker S.E., Holt E.M., Ashburner M., Hienderson S.N.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Hienderson S.N.,
RA Sutron G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Batladon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendala J., Bayraktarolgu L., Basley E.M.,
Ballew R.M., Basu A., Baxendala J., Bayraktarolgu L., Basley E.M.,
Ballew R.M., Basu A., Baxendala J., Bayraktarolgu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendala J., Bayraktarolgu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendala J., Bayraktarolgu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendala J., Bayraktarolgu L., Beasley E.M.,
Ballew R.M., Cavaley S., Dahlker L., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller R., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller H. W., Cadies P.,
RA Burtis K.C., Gabrieliata C.C., Ferraz C., Ferraz C., Ferraz C., Ferraz C.,
RA Burtis M.D., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Burtis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Ajalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Ajalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Mattel B., McIntos T.C., McIecod M.P., McPherson D.,
Retrivor D., Mittel B., McIntos T.C., McIecod M.P., McPherson D.,
Retrivor D.R., Nather S., Nather S., Pull Y., Mattel B., McIntos R., Nusskern D.R., Palazzolo M., Murphy B., Murphy L., Muzny D.M., Wang S., Pala K.,
Shier E.C., Siden-Kamos I., Simpson M., Stupski M.P., Shen H.,
Shiers R.R., Reinfert R., Worley F., Wolley C., Yang S., Yao Q.A.,
R. Shier E.C., Shen-Kamos I., Simpson M., Stupski M.P., Shore E., Shen H.,
Shiers S.R., Roddage T.W., Rollong W., 
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Canton-S; TISSUB=Muscle;
MEDLIND=92113004; Pubmed=1730773;
MEDLIND=92113004; O'Donnell P.T. Heitz J.M., Vito M., Bernstein S.I.;
"Analysis of Drosophila paramyosin: identification of a novel isoform which is restricted to a subset of adult muscles.";
                                                                                                                Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Linsecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92167957; PubMed=1371577; Vinos J., Maroto M., Garesse R., Marco R., Cervera M.; "Drosophila melanogaster paramyosin: developmental pattern, mapping and properties deduced from its complete coding sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Oregon-R;
MEDLINE=91332901; PubMed=1908014;
Vinos J., Domingo A., Marco R., Cervera M.;
"Identification and characterization of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 103-571 FROM N.A., AND CHARACTERIZATION
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Gen. Genet. 231:385-394(1992)
                                                                                                                                                                                                                                                                                                                                                                                       Cell Biol. 116:669-681(1992).
                                                                   long form.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                       NCBI_TaxID=7227;
                                                                                           PRM OR CG5939
                                                                      Paramyosin,
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paramyosin.";
J. Mol. Biol. 220:687-700(1991).

-!- FUNCTURAL COMPONENT OF MANY THICK
-!- FUNCTION: PARAMYOSIN IS A MAJOR STRUCTURAL COMPONENT OF MANY THICK
FILAMENTS ISOLATED FROM INVERTEBRATE MUSCLES.
-!- SUBGNIT: HETERODIMER OF TWO ISOFORMS (POTENTIAL).
-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS, A LONG FORM (SHOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002928; Myosin_tail.
Pfam; PF01576; Myosin_tail; 1.
Coiled coil; Muscle protein; Thick filament; Myosin; Phosphorylation;
                                                                                                                                                                                                                   -!- DEVELOPMENTAL STAGE: UNDETECTABLE DURING GASTRULATION AND BARLY PHASES OF GERM BAND FORMATION. INCREASES DURING ORGANOGENESIS, AROUND 10 HOURS POSTFERTILIZATION, TO THE ADULT STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                           HERE) AND A SHORT FORM (AC P35416); ARE PRODUCED BY ALTERNATIVE SPLICING AND/OR POST-TRANSLATIONAL MODIFICATIONS.
--- TISSUE SPECIFICITY: EXPRESSED IN ALL LARVAL AND ADULT MUSCLE TISSUES. EXPRESSION IS FIVE TIMES HIGHER IN TUBULAR THAN IN FIBRILLAR MUSCLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92316236; PubMed=1618328; Hosaka K., Tanaka S., Nikawa J.-I., Yamashita S.; Hosaka K., Tanaka S., Nikawa J.-I., Yamashita S.; "Cloning of a human choline kinase cDNA by complementation of the yeast cki mutation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NONHELICAL REGION (POTENTIAL).
INTERCHAIN (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85BB333519815A1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Choline kinase (EC 2.7.1.32) (CK) (CHETK-alpha).
                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: HIGH, TO MYOSIN HEAVY CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 456 AA
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003554; AAF50370.1; -. PIR; S20486; S20486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102338 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X58722; CAA41557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternative splicing.
DOMAIN 1
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368
784
500
879 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                             VIVO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KICH_HUMAN
P35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHK OR CKI
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MEDLINE-95208356; PubMed=7900425;
Verhasselt P., Aert R., Voet M., Volckaert G.;
"Twelve open reading frames revealed in the 23.6 kb segment flanking the centromere on the Saccharomyces cerevisiae chromosome XIV right
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piper R.C., Cooper A.A., Yang H., Stevens T.H.;
"VPS27 controls vacuolar and endocytic traffic through a prevacuolar compartment in Saccharomyces cerevisiae.";
J. Cell Biol. 131:603-617(1995).
                                                                             -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                             PATHWAY: INITIAL STEP OF THE CDP-CHOLINE AND CDP-ETHANOLAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
FEBS Lett. 304:229-232(1992).
-!- FUNCTION: MAY HAVE A REGULATORY ROLE IN PHOSPHATIDYLCHOLINE
                                                                                                                                                                                                                                                                                                                                                             ;
0
                                + O-phosphocholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.6%; Score 36; DB 1; Length 456;
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                                                                                                                                                                                                                                                                                                               BD8D13D102178E97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vacuolar protein sorting-associated protein VPS27, VPS27 OR GRD11 OR YNR006W OR N2038.
                                                                                                                                                                                                                                                                                                                                                              .
9
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     622 AA.
                                  CATALYTIC ACTIVITY: ATP + choline = ADP
                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                    -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                         PRO-RICH.
                                                                                                                                                                                                                                                     InterPro; IPR002573; Choline_kinase. Pfam; PF01633; Choline_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=96042307; PubMed=7593183;
                                                                                                                                                                                                                                                                                                                52065 MW;
                                                                                                                                                                                                          EMBL; D10704; BAA01547.1; -.
                                                                                                                                                                                                                                                                                                                                                  38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                           386 QNDFENLSTEEKSIIKEE 403
                                                                                                                                                                                                                                                                                                                                                                                    1 KNTMEHVXXXEESIIXQE 18
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 38.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                     303
                                                                                                                                                                                                                   PIR; S23104; S23104.
Genew; HGNC:1937; CHK.
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                                                                                                                                                                                                                                                                                                                456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                       SYNTHESIS.
                                                         PATHWAYS.
                                                                                                                                                                                                                                           MIM; 118491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VP27_YEAST
P40343;
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                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Guanosine-3',5'-bis(Diphosphate) 3'-pyrophosphohydrolase (EC 3.1.7.2)
((ppgpp)ase) (Penta-phosphate guanosine-3'-pyrophosphohydrolase).
SPOT
There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutant of Spiroplasma citri.";
J. Bacteriol. 179:4802-4810(1997).
-!-FUNCTION: IN BUBACTERIA PREPP (GUANOSINE 3'-DIPHOSPHATE 5-'DIPHOSPHATE) IS A MEDIATOR OF THE STRINGENT RESPONSE THAT COORDINATES A VARIETY OF CELLULAR ACTIVITIES IN RESPONSE TO CHANGES IN UTRITIONAL ABUNDANCE. HIS ENZARE CATALYSES THE DEGRADATION OF PROEP INTO GDP. IT MAY ALSO BE CAPABLE OF CATALYZING THE SYNTHESIS OF PROEP (BY SIMILARITY).
-!-CATALYZING ACTIVITY: Guanosine 3',5'-bis(diphosphate) + H(2)O guanosine 5'-diphosphate + diphosphate.
-!-COFACTOR: MANGANESE (BY SIMILARITY).
-!-SIMILARITY: BELONGS TO THE RELA / SPOT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jacob C., Nouzieres F., Duret S., Bove J.M., Renaudin J.; "Isolation, characterization, and complementation of a motility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.6%; Score 36; DB 1; Length 622; 58.3%; Pred. No. 46; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NV -> KL (IN REF. 2).
022C23CBAB2E7E1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FYVE-TYPE.
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=GII-3;
MEDLINE=97386419; PubMed=9244268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHS.
                                                                                                                                                                                                                                                                                                     InterPro; IPR002014; HRS.
InterPro; IPR002950, Josephin.
InterPro; IPR003903; UIM.
InterPro; IPR003905; Znf_FYVE.
Pfam; PF00790; VHS; 1.
Pfam; PF01363; FYVE; 1.
Pfam; PF01363; FYVE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spiroplasmataceae; Spiroplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70945 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50178; ZF_FYVE; 1. PROSITE; PS50179; VHS; 1.
                                                                                                                                                             EMBL; U24218; AAA96002.1; -. EMBL; X77395; CAA54574.1; -.
                                                                                                                                                                                                                       Z71620; CAA96282.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD003686; HRS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 58.3 nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00064; FYVE; 1.
SMART; SM00288; VHS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 DIMEHVILREDS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NTMEHVXXXEES 13
                                                                                                                                                                                                                                                 PIR, S45129; S45129.
SGD; S0005289; VPS27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321
622 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spiroplasma citri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPOT_SPICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
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InterPro; IPR004811; Spor_relA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GTP pyrophosphokinase (EC 2.7.6.5) (APP:GTP 3'-pyrophosphotransferase)
(PPGPP synthetase I) ((P)PPGPP synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harris B.Z., Kaiser D., Singer M.H.;
"The guanosine nucleotide (p)ppGpp initiates development and A-factor production in Myxococcus xanthus.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: IN EUBACTERIA PPGPP (GUANOSINE 3'-DIPHOSPHATE 5-'
DIPHOSPHATE) IS A MEDIATOR OF THE STRINGENT RESPONSE THAT
COORDINATES A VARIETY OF CELLULAR ACTIVITIES IN RESPONSE TO
CHANGES IN NUTRITIONAL ABUNDANCE. THIS ENZYME CATALYSES THE
FORMATION OF PPPGPP WHICH IS THEN HYDROLYSED TO FORM PPGPP (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY),
CATALYTIC ACTIVITY: ATP + GTP = AMP + guanosine 3'-diphosphate 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     triphosphate.
--- PATHWAY: FIRST STEP IN THE METABOLISM OF PDGPP.
--- SIMILARITY: BELONGS TO THE RELA / SPOT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 1; Length 749;
Pred. No. 56;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                                                        86281 MW; D32992E612317042 CRC64;
                                                                                                                                                                     InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR004811; SpoT_relA.
InterPro; IPR004095; TGS_dom.
Pfam; PF01842; ACT; 1.
Pfam; PF01966; HD; 1.
                                                                                                                                                                                                                                                           Pfam; PF02824; TGS; 1.
SMART; SM00471; HDc; 1.
TIGRFAMS; TIGR00691; spor_relA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002819; HD.
InterPro; IPR003607; ME_Pplase_HDc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF025847; AAB97677.1; -.
                                                                                                             EMBL; U89875; AAC45548.1; -.
InterPro; IPR002912; ACT.
InterPro; IPR002819; HD.
                                                                                                                                                                                                                                                                                                                                                                              39.68;
                                                                                                                                                                                                                                                                                                                                                                                              38.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 LENISVQERDEIQQEVYK 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 MEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 38.99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002912; ACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                     Hydrolase; Manganese.
SEQUENCE 749 AA; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-DK101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RELA_MYXXA
                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Gaps
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                                                                                                                         DB 1; Length 757; 56;
                                                                                                                                                        5; Indels
                                                                                                     84978 MW; D6CC1000A5F72A7B CRC64;
                                                                                                                                                     6; Mismatches
                                                                                                                                                                                                                                           Search completed: February 11, 2003, 18:17:48 Job time: 11.3093 secs
                                                                                                                           Score 36;
Pred. No.
        Interpro; IPR004095; TGS_dom.
Pfam; PF01842; ACT; 1.
Pfam; PF01966; HD; 1.
Pfam; PF02824; TGS; 1.
SMART; SM00471; HDc; 1.
TIGRFAMS; TIGR00691; SP0T_relA; 1.
                                                                                                                             39.6%;
35.3%;
                                                                                                                                                                                                       167 TLDHMSEEKQARIAQET 183
                                                                                                                                      Best Local Similarity 35.3
Matches 6; Conservative
                                                                                                                                                                               3 TMEHVXXXEESIIXQET 19
                                                                                      Transferase; Kinase.
SEQUENCE 757 AA;
                                                                                                                             Query Match
Qγ
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 11, 2003, 18:13:41; Search time 23.5979 Seconds Run on:

(without alignments)
183.363 Million cell updates/sec

US-09-380-738A-4 91

1 KNTMEHVXXXEESIIXQETYK 21 Perfect score: Sequence:

671580 segs, 206047115 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_21:* Database

sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_vertebrate:*
sp_unclassified:* sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:* sp_bacteriap:* sp_archea:* sp_bacteria:* sp_archeap:* sp_rvirus:* sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
τ.	82	90.1	210	9	062825	062825 bubalus bub
7	53.5	58.8	124	9	Q9MYU7	Q9myu7 capra hircu
æ	53.5	58.8	223	9	Q9TTQ7	
4	53.5	58.8	223	9	Q9GK07	
ស	52.5	57.7	223	9	O9MYU6	Q9myu6 capra hircu
9	43	47.3	953	4	9dIn60	Q9uld6 homo sapien
7	42	46.2	266	7	032309	032309 bacillus th
80	40.5	44.5	334	16	Q9PK31	Q9pk31 chlamydia m
6	40	44.0	300	16	Q9KDH5	Q9kdh5 bacillus ha
10	39.5	43.4	333	16	09JS73	091s73 chlamydia p
11	39.5	43.4	333	16	Q926L1	09z611 chlamydia p
12	39	42.9	235	6	Q8SCS9	Q8scs9 pseudomonas
13	39	42.9	2206	Ŋ	096205	096205 plasmodium
14	38.5	42.3	2647	2	Q9U4X0	Q9u4x0 plasmodium
15	38	41.8	176	7	052510	052510 enterobacte
16	38	41.8	176	7	Q47257	Q47257 escherichia

Q93fkl citrobacter Q977k6 uncultured Q9vym8 drosophila Q9u399 caenorrhabdi O59719 pseudomonas	L L U		Q9fjkl arabidopsis Q9c5y4 arabidopsis Q9tuy9 arabidopsis Q9tut9 homo sapien Q95752 homo sapien Q9ttj3 homo sapien Q8t6h2 dictyosteli Q9u8m0 periplaneta Q80072 staphylococ
203 2 Q93FK1 217 1 Q977K6 242 5 Q9VXM8 320 5 Q91399 396 2 O59719	11 11 10 10 12 16 16	200000	1175 10 Q9FJK1 1175 10 Q9FGY4 1177 10 Q9FUY9 1202 4 Q9UNT9 1288 4 Q9ST52 1288 4 Q9NTJ3 1308 5 Q9UEH2 1896 5 Q9UEM0 91 9 Q80072
38 41.8 2 38 41.8 2 38 41.8 2 38 41.8 3	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		37 40.7 111 37 40.7 111 37 40.7 12 37 40.7 12 37 40.7 12 37 40.7 12 37 40.7 12 36 39.6
10 20 30 30 30 30		2 3 3 3 3 3 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6	7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

ALIGNMENTS

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Gaps
                                                                                                         ASS-casein (Fragment).

Bubalus bubalis (Domestic water buffalo).

Bubalus bubalis (Comestic water buffalo).

Bubaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bubalus.
                                                                                                                                                                                                                                                                         Β.
                                                                                                                                                                                                                                      TISSUE-MAMMARY GLAND,
Das P., Jain S., Garg L.C.;
Das P., Jain S., Garg L.C.;
Cloning and nucleotide sequence of cDNA encoding aS2-casein in luctalis.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ005431; CAA06534.2; -
InterPro; IPR001588; Casein.
Pfam; PF00363; caseins; 2.
NON_TER
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0
                                                                                                                                                                                                                                                                                                                                                                                                                   90.1%; Score 82; DB 6; Length 210; 76.2%; Pred. No. 1.2e-07; Live 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                        NON_TER 1 1
SEQUENCE 210 AA; 24700 MW; 05DEF95963F1132C CRC64;
                                                          01-AUG-1998 (TrEMBLrel. 07, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                              210 AA
                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KNTMEHVXXXEESIIXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 KHTMEHVSSSEESIISQETYK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                               062825
RESULT 1
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; 0

124 AA.

PRT;

PRELIMINARY;

Q9MYU7; Q9MYU7;

AC AC

RESULT 2 Q9MYU7

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1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                 Capra hircus (Goat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capra hircus (Goat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.8%; Score 53.5; DB 6; Length 124; 59.1%; Pred. No. 0.018; 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.8%; Score 53.5; DB 6; Length 223; 59.1%; Pred. No. 0.034; ive 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                 Lagonigro R., Pilla F., Matassino D., Zullo A.;
Lagonigro R., Pilla F., Matassino D., Zullo A.;
"Sequence of goat alpha s2-casein allele 0 encoding cDNA.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ289715; CAB94235.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Veltri C.C., Pilla F.F., Lagonigro R.R.;
"A new allele of goat alpha s2-casein.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ249995; CAB59920.1;
InterPro; IPR001588; Casein.
Pfam; PF00363; Caseins; 2.
PROSITE; PS00366; CASEIN.ALPHA_BETA; 1.
SEQUENCE 223 AA; 26433 MW; CE9F4DC8D7688293 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR01588; Casein.
PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
SEQUENCE 124 AA; 14533 MW; C363E536CCI7B5F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                      Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 AA
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           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KNTMEHVXXXEESI-IXQETYK 21
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01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                            Alpha s2-casein.
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CSN1S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Boyoidea;
            Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                          Length 223;
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                                                                                                                                                                                                                                                                                                                                                        Score 53.5; DB 6; Length 2
Pred. No. 0.034;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Lagondaro R., Pilla F., Matassino D., Zullo A.;
Lagondaro R., Pilla F., Matassino D., Zullo A.;
"A new allele of goat alpha s2-casein gene.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ28916; CAB94236.1;
InterPro; IPR001588; Casein.
Pfam; PF00363; caseins; 2.
Prosite; PS00306; CASEIN_ALPHA_BETA; 1.
PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                             SEQUENCE FROM N.A.
Veltri C., Pilla F., Lagonigro R.;
Veltri C., Pilla F., Lagonigro R.;
Submitted of Jan-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ297310; CAC21704.2;
EMBL; AJ297311; CAC21704.2;
                                                                                                                                                                                                                                                                                                                 CASEIN_ALPHA_BETA; 2.; 26432 MW; CE9765E8D7688C9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
Alpha s2-casein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.7%; Score 52.5; DB 6;
54.5%; Pred. No. 0.053;
live 2; Mismatches 7;
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                                                                                                                                                               JOINED.
                                                                                                                                                AJ242728; CAC21704.2; JOINED. AJ297312; CAC21704.2; JOINED. AJ297313; CAC21704.2; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                               1 KNTMEHVXXXEESI-IXQETYK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                        16 KHKMEHVSSSEEPINIFQEIYK 37
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                                                                                                                                                                                                                                                                                                                                                         58.8%;
                                                                                                                                                                                       EMBL; AJ297314; CAC21704.2;
EMBL; AJ242527; CAC21704.2;
EMBL; AJ297315; CAC21704.2;
EMBL; AJ297316; CAC21704.2;
                                                                                                                                                                                                                                                                                      interPro; IPR001588; Casein.
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                                                                                                                                                                                                                                                          EMBL; AJ242528; CAC21704.2;
EMBL; AJ242533; CAC21704.2;
                                                                                                                                                                                                                                               AJ242526; CAC21704.2;
                                                                                                                                                                                                                                                                                                   Pfam; PF00363; caseins; 2. PROSITE; PS00306; CASEIN_A
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 59.19
            Mammalia; Eutheria; Cetari
Bovidae; Caprinae; Capra.
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NCBL_TaxID=9925;
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Best Local Similarity 54.5
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                              223 AA;
                                     NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9MYU6;
Q9MYU6;
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Q9ULD6;
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                                                                                                                                                                                                                               EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                             "Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XV.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:337-345(1999).
EMBL; AB033110; BAA86598.1; -.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmičutes; Bacillus/Clostridium group; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.3%; Score 43; DB 4; Length 953; 42.1%; Pred. No. 16;
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46.2%; Score 42; DB 2; Length 566;
Best Local Similarity 40.0%; Pred. No. 14;
Matches 8; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                953 AA; 106788 MW; 96107F4A7EEBAB2C CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
KIAA1284 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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EMBL; L77763; AAB62279.1; -.
HSSP; P05806; 1NPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      566 AA
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PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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InterPro; IPR001570; Peptidase_M4.
InterPro; IPR005075; Pep_M4_propep.
InterPro; IPR000130; Zn_MPeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                           MEDLINE=20039619; PubMed=10574462;
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Pfam; PF02868; Peptidase_M4_C; 1.
Pfam; PF03413; Pep_M4_propep; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97316439; PubMed=9172350;
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les 8; Conservative
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PROSITE; PS50106; PDZ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 01-JAN-1998 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus thuringiensis.
                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neutral protease A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             crystal protein.";
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Read T.D., Brunham R.C., Shon C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.
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EMBL, AP001511; BaBd4957.1; --
InterPro; IPR002524; Cation_efflux.
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NCBI_TaxID-86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.5%; Score 40.5; DB 16; Length 334; 50.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., M.
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 AA; 36718 MW; 1FE91A6EFB4633E0 CRC64;
                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Aspartate-semialdehyde dehydrogenase.
TC0642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                              Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
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                                                                                                                                        334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 16;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
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STRAIN-MOPN / NIGG;
MEDLINE-20150255; PubMed-10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: JP800534; Semialdh_dh. Pfam; PF01118; Semialdhyde_dh; 1. Pfam; PF02774; Semialdhyde_dhc; 1. TIGRFAMS; TIGR00978; asd_EA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE002332; AAF73580.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 NTIPHILGEEEK-IHQETLK 205
                       221 NTIDHVTNDDKSPVKQEAPK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 NTMEHVXXXEESIIXQETYK 21
2 NTMEHVXXXEESIIXQETYK 21
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                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                 Chlamydia muridarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 334 AA;
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Q9KDH5
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Q9PK31
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STRAIN-AR39;

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EMBL, APO02548; BAS99255.1; DitterPro; IPRO00544; Semialdh.d. Pfam; PF01118; Semialdhyde.dh; 1. Pfam; PF02774; Semialdhyde.dh; 1. SEQUENCE 333 AA; 37316 MW; 163C27693662B7A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ASPATATE dehydrogenase (Aspartate-semialdehyde dehydrogenase).
ASD OR CPN1048 OR CP0804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 333;
                                                                                   / Match 44.0%; Score 40; DB 16; Length 300; Local Similarity 35.0%; Pred. No. 17; Onservative 6; Mismatches 7; Indels
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                                                    300 AA; 32794 MW; 876DF4C44387D35E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83558;
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                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.4%; Score 39.5; DB 16;
45.0%; Pred. No. 24;
tive 4; Mismatches 6;
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                                                                                                                    6; Mismatches
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MEDLINE=99206606; PubMed=10192388;
Pfam; PF01545; Cation_efflux; 1.
TIGRFAMs; TIGR01297; CDF; 1.
                                                                                                                                                                          212 NTLDHVLHDEDTVEMREAAK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||: |: || |: || |
185 NTVPHIVGEEEKIL-RETVK 203
                                                                                                                                                   2 NTMEHVXXXEESIIXQETYK 21
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                                                                                                                                                                                                                                                                                                                                                     Aspartate dehydrogenase.
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                                    Complete proteome. SEQUENCE 300 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=J138
                                                                                     Query Match
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Matches
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         MEDLINE-20150255; PubMed=10684935; Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Elsen J., Fraser C.M.; Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39."; Nucleic Acids Res. 28:1397-1406(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
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                                                                                                                                                                                                                                                                                                                                                      43.4%; Score 39.5; DB 16; Length 333; 45.0%; Pred. No. 24; tive 4; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.9%; Score 39; DB 9; Length 235; 44.4%; Pred. No. 21;
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                                                                                                                                                                                                                                                                                                                      333 AA; 37300 MW; 105DC76938D8B7A7 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pfam. PF01118; Semialdhyde_dh; 1.
Pfam. PF02774; Semialdhyde_dh; 1.
IIGRFAMF; TIGR00978; asG_EA; 1.
                                                                                                                                                                        EMBL; AE001685; AAD19185.1; -. EMBL; AE002239; AAF73704.1; -. TIGR; CP0804; -.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas phage phiKZ.
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                    Complete proteome. SEQUENCE 333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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MEDLINE=99021743; PubMed=9804551;

MEDLINE=99021743; PubMed=9804551;

Gardner M.J., Tettelln H., Carucci D.J., Cummings L.M., Aravind L.,

Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,

Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M.,

Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,

Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;

"Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                          Gaps
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        falciparum, maps within a favored linkage group in two genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=20078864; PubMed=10613703;
Peterson D.S., Wellems T.E.;
"EBL-1, a putative erithrocyte binding protein of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
              Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                         Score 39; DB 5; Length 2206; Pred. No. 2.2e+02; 3; Mismatches 9; Indels
                                                                                                                                                              304550 MW; AE98F88FD754E300 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative erythrocyte binding protein EBL-1 (Fragment).
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EAEIM-B.
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Lee K.F., Shaw P.C., Picone S.J., Wilson G.G., Lunnen K.D.;
Lee K.F., Shaw P.C., Picone S.J., Wilson G.G., Lunnen K.D.;
Sequence comparison of the EcciK311 and East restriction modification
                                                                                                                                                                                                                                                        Gaps
                                                                                          systems suggests an intergenic transfer of genetic material."; Biol. Chem. 379:437-441(1998).
EMBL; AF039582; AAB95337.1; -.
Methyltransferase; Transferase.
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                                                                                                                                                                                                              41.2%; Score 38; DB 2; Length 176;
41.2%; Pred. No. 24;
Live 3; Mismatches 7; Indels
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91.669 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			1D Description	AAW56195 Anti-inflammator	AAW56182 Anti-inflammatory	AAW78378 Isoelectric focus	ABB47202 OB-cadherin CAR pe	AAP60670 Sequence of amino	AAP60497 Peptide with FC r		AAR52607 Inhibitor of signa		
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AAY-1997; 97US-0864301. SEP-1996; 96US-0025376. AOV-1996; 96US-0733141. DA) YEDA RES & DEV CO LTD. PETMAN P, Eisenbachschwartz M, Hirschberg DL; 1998-193550/17.	SEP-19	; 97WO	-IL00	1295.		
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                                                                      They are derived from the formulae.

Xaa Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
Xaa any amino acid residue.

Cyclic derivatives of the peptides also function as anti-inflammatory agents. The peptides can be covalently linked to one another either directly or through a spacer. The peptides and their derivatives have macrophage inhibitory and T-cell inhibitory activity and thus, anti-inflammatory activity. The peptides and compositions have anti-inflammatory activity. The peptides and compositions have anti-inflammatory activity in- inhibitory effects against a cellular and humoral immune response, including a response not associated with inflammation. The peptides also inhibit the ability of macrophages and T-cells to adhere to extracellular matrix components and fibronectin, as well as up-regulated fas receptor expression in T-cells. They can be used to inhibit unwanted immune reaction and inflammation.
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Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
                                                             AAW56171-248 represent anti-inflammatory tripeptides of the invention
                                                                                                                                                                                                                                                                                                                  Gaps
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arthritis, ulcerative colitis, auto-immune disease, allergy asthma, shock, HIV infection, transplant rejection or Alzheimer's disease
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                                    Claim 5; Page 34; 42pp; English.
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96US-0753141.
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Naa = any amino acid residue.

Cyclic derivatives of the peptides also function as anti-inflammatory agents. The peptides can be covalently linked to one another either addirectly or through a spacer. The peptides and their derivatives have macrophage inhibitory and T-cell inhibitory activity and thus, anti-inflammatory activity. The peptides and compositions have anti-immune activity, i.e. inhibitory effects against a cellular and humoral immune response, including a response not associated with inflammation. The peptides also inhibit the ability of macrophages and T-cells to adhere to extracellular matrix components and fibronectin, as well as up-regulated fas receptor expression in T-cells. They can be used to inhibit unwanted immune reaction and inflammation.
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW78378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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AAP60497;
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hahn GS;
                                                                                                                                                                            (ANDE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP60497
Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         öλ
                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, comprising a modulating agent comprising a desmosomal cadherin cell adhesion recognition CAR sequence (ABB47341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR sequence, a substance such as an antibody or antigen-binding fragment that specifically binds a desmosomal cadherin CAR sequence and/or a polynucleotide encoding a polypeptide that comprises a desmosomal cadherin CAR sequence or analogue. The modulating agents have immunosuppressive, cytostatic and antiapoptotic activity and are used to facilitate wound healing and/or reduce scar tissue, for enhancing adhesion of foreign tissue implants (e.g. skin graft or organ implant), treating an autoimmune blistering disorder and to treat cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                              Modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, useful for facilitating wound healing and/or reducing scar tissue, treating cancer and inducing apoptosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                     Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive; cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of amino terminal extension 3 for recombinant human growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.9%; Score 10; DB 23; Length 3; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 50; 127pp; English
                                                                                                                                                                                                                                                                                                                   Gour BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP60670 standard; Protein; 4 AA.
                               ABB47202 standard; Peptide; 3 AA.
                                                                                                                                                                                                                                                                                             (ADHE-) ADHEREX TECHNOLOGIES INC
                                                                                                                                                                                                                                                27-MAR-2001; 2001WO-IB01400.
                                                                                                                                                                                                                                                                       27-MAR-2000; 2000US-0535852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (updated)
(first entry)
                                                                                                 OB-cadherin CAR peptide 15.
                                                                           30-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                   Blaschuk OW, Symonds JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                         WPI; 2002-025778/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AA;
                                                                                                                                                                                                   WO200172956-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2002
26-JUL-1991
                                                                                                                                                                                                                          04-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ~
                                                                                                                                                           apoptosis.
                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP60670;
                                                      ABB47202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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EE
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AAP60670
XX
AC AAP6
XX
DT 03-O
DT 26-J
XX
DE Sequ
         RESULT 4
                     ABB47202
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human growth hormone prodn. - by reacting amino terminal extended hormone with d1:peptidyl aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino terminal extension is cleaved selectively and in a high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yield and the formed hGH may then easily be separated from any residues of partly converted amino terminal extended hGH by anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
hormone, cleavable with dipeptidyl aminopeptidase I (DAP I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.9%; Score 10; DB 7; Length 4; 100.0%; Pred. No. 7.8e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hansen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antiinflammatory; antiallergic; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Updated on 03-OCT-2002 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide with Fc receptor-blocking activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Christensen T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 4; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP60497 standard; protein; 4 AA.
                                               Recombinant human growth hormone.
                                                                                                                                                                                                                                                                                                                                                                                       NORDISK GENTOFTE A/S
                                                                                                                                                                                                                               86WO-DK00014.
                                                                                                                                                                                                                                                                                                                                               (NGEN-) NORDISK GENTOFTE AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84WO-EP00242
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                                                                                                                                                                                                                                                                          85DK-0000556.
88DK-0003482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pedersen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                         (NOGE-) NORDISK GENTOFTE (NOVO ) NOVO-NORDISK A/S
                                                                                                                                                                                                                                                                                                                                                                      ANDERSEN H D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1986-225461/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1986-068963/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
hes 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MERE ) MERCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-AUG-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-AUG-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andersen H,
                                                                                                                                                                                                                                                                                               24 - JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-1991
                                                                                                                                       WO8604609-A.
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                                                                                                                                                                                    14-AUG-1986
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92GB-0011668,

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02-JUN-1992;
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AAR52607
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                                                                                                                                                                                                                                                                                                                        the calpha atom, or together with RD forms an alkylidene group, or is H where one of RA, RA' RD and RE is other than hydrogen"
                                                                                                                                  Gaps
                                                  The sequence is an active-site compound which blocks immune-complex binding to Ig Fc receptors and/or Ig binding to lymphocyte Fc receptors. The peptide modulates immune complex-mediated immunosuppression, inflammation and tissue disruption, and reduces human allergic responses.
                                                                                                                                 0;
                                                                                                                                                                                                                                                               Hemoregulatory peptide; inhibition; cell division;
myelopoietic cells; bone marrow cells; proliferation; cancer;
autoimmune disease; psoriasis; antibody; immunoassay.
      New active site peptide derivs. - blocking binding of immune complex or immunoglobulin to Fc receptors, useful e.g. for
                                                                                                                76.9%; Score 10; DB 7; Length 4; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
                                     Claim 22; Page 78-79; 87pp; English.
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                   AAR44299 standard; peptide; 4 AA.
                      treating auto-immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93WO-GB01172
                                                                                                                                                                                                                                 (first entry)
                                                                                                                                Conservative
                                                                                                                                                                                                                                                Heamoregulatory peptide
                                                                                                                                                                                                                                                                                                                    3
∕note≕
                                                                                                                        Local Similarity
les 2; Conserv
                                                                                                 4 AA;
                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                 13-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-DEC-1993
                                                                                                                                              4 EE 5
                                                                                                                                                             EE 4
                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                   Seguence
                                                                                                                                                                                                                  AAR44299;
                                                                                                                Query Match
                                                                                                                                Matches
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δλ
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Gaps
                                                                                                                                                                                                                   This sequence represents a hemoregulatory peptide compound derivative. Peptides based on this sequence may be used for inhibiting cell division,particularly myelopoietic or bone marrow cells. They can be used to inhibit proliferation of cells in the treatment of cancer, autofimmune diseases or psoriasis. They may also be used to generate antibodies for use in immunoassays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide(s) contg. tyrosine or phosphorylated analogues - used
                                                                                                                 Single-chain haemo-regulatory peptide derivs. - useful for inhibiting proliferation of cells, partic. myelopoietic and bone
                                                                                                                                                                                                                                                                                                                                                                                                          ó.
                                                                                                                                                                                                                                                                                                                                                                       76.9%; Score 10; DB 14; Length 4; 100.0%; Pred. No. 7.8e+05; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          __note= "phosphonomethylphenylalanine
    or mono- or difluorophosphono-
    methylphenylalanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal transduction; phosphonomethylphenylalanine; monofluorophosphonomethylphenylalanine; difluorophosphonomethylphenylalanine; kinase; enzyme; protein tyrosine phosphatase; PTPase; SH2-domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hydrolysis resistant; phosphorous; diabetes; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                     Claim 11; Page 46; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR52607 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibitor of signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (JOSL-) JOSLIN DIABETES CENT.
(HAFS-) HAFSLUND NYCOMED AS. (HOLM/) HOLMES M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93WO-US09626
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                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                 WPI; 1993-405729/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-150930/18.
                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                         4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                    marrow cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-OCT-1993;
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                                                Undheim K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              malignancy
                                                                                                                                                                                                                                                                                                                                                                                                                                         4 EE 5
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                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                               Gaps
for inhibiting the dephosphorylation of a substrate by a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compounds displaying a surface similar to the surface presented by one of five distinct lateral domains of {\tt CD4} - inhibit T cell
                                                                 A peptide capable of inhibiting the interaction of a SH2-domain contg. protein with a second protein comprises sequence (I) R1-R2-R3-R4 (I)
                                                                                                                                                                                                                             processes, e.g. abnormal processes associated with diabetes and for treating selected malignancies. They can also be used to study the enzymatic mechanisms of Prpase activity and to investigate the metabolic and biochemical roles of PrPases.
                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                    R4= 116, Met. Leu or Val.
Examples of such peptides are given in AAR52607-19.
The peptides can be used for inhibiting cellular protein
tyrosine phosphatases (PTPases) and for controlling metabolic
                                                                                                              R1= Tyr, phosphotyrosine or an analogue of phosphotyrosine
                                                                                                                                                                                                                                                                                                                                  Length 4;
                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                         having a hydrolysis resistant phosphorous molety; R2= Asp, Thr, Tyr, His, Gln, Met, Val, Ile or Glu; R3= any amino acid;
                                                                                                                                                                                                                                                                                                                               Score 10; DB 15; 1 Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jameson BA, Korngold R, Mcdonnell JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDR3 region of L3T4 peptide mimic.
                                                                                                                                                                                                                                                                                                                     76.9%; Sco.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR55019 standard; peptide; 4 AA
                                         Claim 12; Page 57; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 50; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93WO-US10999,
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                                                                                                                                                                                                                                                                                                                                                             Conservative
              tyrosine phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-183151/22.
                                                                                                                                                                                                                                                                                                                                              Local Similarity les 2; Conserv
                                                                                                                                                                                                                                                                                                    4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYJE-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                          EE 5
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                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      EE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR55019;
                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
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A molecular model of the mouse CD4 protein (L3T4) was developed from the high resolution crystal structure of human CD4 (Brookhaven

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CD4; Complementarity determining regions; CDR; lateral domains; mimics; glycoproteins; Immunoglobulin superfamily; SLE; MS; RA; GVH; inhibit T cell proliferation; treatment of multiple sclerosis; systemic lupus erythematosus; graft rejection; rheumatoid arthritis; graft versus host disease; T cell leukaemias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from the high resolution crystal structure of human CD4 (Brookhaven code: 1CD4). The CDR regions were used for modelling peptide minics CD4: The CDR regions were used for modelling peptide minics or 90-92 (Lys Glu Glu) of CD4 and may comprise additional flanking sequences from CD4. This peptide comprises amino acids 90-93. The peptide minics are useful for inhibiting the proliferation of T cells modulating immune responses in mammals and may be used to treat, e.g. SLE, RA, MS, GVH, graft rejection and T cell leukaemias,
code: 1CD4). The CDR regions were used for modelling peptide mimics. CDR3 peptides comprise the essential amino acids 88-90 (Asp Gln Lys) or 90-92 (Lys Glu Glu) of CD4 and may comprise additional flanking sequences from CD4. This peptide comprises amino acids 89-92. The peptide mimics are useful for inhibiting the proliferation of T cells modulating immune responses in mammals and may be used to treat, e.g. SLE, RA, MS, GVH, graft rejection and T cell leukaemias,
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compounds displaying a surface similar to the surface presented by one of five distinct lateral domains of CD4 - inhibit T cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecular model of the mouse CD4 protein (L3T4) was developed
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                                                                                                                                                                                          Length 4;
                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                        DB 15, I
7.8e+05;
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                                                                                                                                                                                       76.9%; Score 10; DB 100.0%; Pred. No. 7.8 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jameson BA, Korngold R, Mcdonnell JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDR3 region of L3T4 peptide mimic.
                                                                                                                                                                                                                                                                                                                                                                                AAR55021 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.98;
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93US-0076092.
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                                                                                                                                                                                                                            Conservative
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Matches 2; Conserv
                                                                                                                                                         4 AA;
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                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Intracellular binding of antigens - by using antibody targetting with vector system, for \text{e.g.}\ \text{tumour suppression}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New vector systems comprise a sequence adapted for intracellular
                         0;
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                                                                                                                                                                                                                                   Single chain antibody; sFv; heavy chain; light chain; kappa; variable domain; hydrophilic linker; antibodies; endoplasmic reticulum retention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4;
                         Indels
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Pred. No. 7.8e+05;
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                             Endoplasmic reticulum retention signal DEEL.
                                                                                                                                                                                                                                                                                                                                                                                                                         (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 32; Page 100; 155pp; English
                                                                                                                                   AAR48248 standard; peptide; 4 AA.
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                        ;
           100.08;
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                                                                                                                                                                                                                                                                                                                                                                                     92US-0916939
                                                                                                                                                                                    (first entry)
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                        Conservative
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les 2; Conserve
          Best Local Similarity
Matches 2; Conserv
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17-MAR-1993;
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                                              4 EE 5
11
2 EE 3
                                                                                                                                                                                                                                                                                     Synthetic
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The nucleotide and deduced aa sequences of human transducin-like enhancer of split proteins TLE-1 (AAG62175, AAR51476), TLE-2 (AAG62176, AAR51477), TLE-3 (AAG62177, AAR51478) and TLE-4 (AAG62178, AAR51479) were determined. The aa sequences were compared with that of Drosophila E(spl)m9/10 protein (AAR51481). Comparison of the WD-40 domains of these proteins defined the consensus residues shown in AAR51480. The antigen, human c-myc, human p53, human A-myb and dorsal proteins with respect to nuclear localization site, and casein-kinase II and cdc. kinase phosphorylation sites (sequences AAR51482-96). TLE can be used to treat or diagnose (pre)neoplastic conditions, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p53; CK II; casein-kinase II; phosphorylation; CcN motif; transducin-like enhancer of split protein; TLE; cell fate; differentiation; cervix cancer; breast cancer; psoriasis; baldness.
                                                                                                                                                                                                                                                                                                                                New human trainsducin-like enhancers of split protein - and associated multi-protein complexes, chimeric proteins, antibodies, nucleic acid, etc., involved in nuclear-cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
             p53; CK II; casein-kinase II; phosphorylation; CcN motif; TLE; transducin-like enhancer of split protein; protein transport; differentiation; cervix cancer; dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                           Stifani
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                                                                                                                                                                                                                                                                           Redhead NJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. ...
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                                                                                                                                                                                                                                                                          Hill RE,
                                                                                                                                                                                                   92US-0955011.
                                                                                                                                                                        93WO-US09333.
                                                                                                                                                                                                                                (MEDI-) MEDICAL RES COUNCIL.
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                                                                                                                                                                                                                                                                        Artavanis-tsakonas S,
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Matches 2; Conserva
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                                                                                                                                                                                                                                                                                                                                                                             protein transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 AA;
                                                                                                                                                                        30-SEP-1993;
                                                                                                                                                                                                     30-SEP-1992;
                                                                                    Homo sapiens
                                                                                                                                             14-APR-1994.
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                                                                                                               WO9408037-A.
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                                                          malignancy.
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This peptide is a specific example of a generic formula covering 2-amino-6,7-dihydroxy-4-thiaheptanoic acid derivs. bonded to a sequence of 1-10 amino acid residues, at least one of which has a water-solubility enhancing group. Such compounds improve the state of haematopoiesis-insufficiency and can be used for treating or preventing leukocytopaenia caused by radiotherapy or chemotherapy of cancers. They can also be used as haematopoietic stimulating agents in the case of bone marrow transplantation, as immunostimulating agents having leukocyte-increasing action; and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunostimulant; thrombocytopaenia; haematopoiesis insufficiency;
                                                                   New 2-amino-6,7-di:hydroxy-4-thia-heptanoic acid derivs. - are immuno-stimulating agents useful for treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New 2-amino-6,7-di:hydroxy-4-thia-heptanoic acid derivs. - are
                                                                                                                                                                                                                                                                                                         Score 10; DB 15; Lengtn 4,
Pred, No. 7.88+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -amino-6,7-dihydroxy-4-thiaheptanoic acid; bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yukishige K;
                 Yukishige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2-amino-6,7-dihydroxy-4-thiaheptanoic acid deriv.35.
                 Wakimasu M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wakimasu M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                         Example 42; Page 81; 89pp; English.
                                                                                                                                                                                                                                                                                                              76.9%; Scc.
100.0%; Pre
0; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR59899 standard; peptide; 4 AA.
                 Hida T, Tanida S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92JP-0349062.
93JP-0056185.
93JP-0181735.
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                                                                                                                                                                                                                                                                     treating thrombocytopaenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                          WPI; 1994-210219/26.
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                                                                                              thrombocytopenia
                                                                                                                                                                                                                                                                                               4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
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22-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-1992;
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                 Harada S,
                                                                                                                                                                                                                                                                                                                                                                                          3 EE 4
                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
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                                                                                                                                                                                                                     The nucleotide and deduced as sequences of human transducin-like enhancer of split proteins TLE-1 (AAQ45333, AAR51109), TLE-2 (AAQ45334, AAR51110), TLE-3 (AAQ45335, AAR51111) and TLE-4 (AAQ45336, AAR52953) were determined. The as sequences were compared with that of Drosophila E(spl) m9/10 (AAR52955). Comparison of the WD-40 domains of these proteins defined the consensus residues shown in AAR52954. The CCN motifs of the proteins were compared with those of SV40 T antigen, human c-myc, human B33, human A-myb and dorsal protein with respect to nuclear localization site, and casein-kinase and cd2-kinase phosphorylation sites (sequences AAR52956-70).
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                         Transducin-like enhancer or split proteins and nucleic acids-are for treatment of disorders of cell fate or differentiation e.g. cervical cancer, breast cancer, psoriasis, baldness etc.
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                                                                                                                                                                                                                                                                                                                                                                           76.9%; Score 10; DB 15; Lengtn 4,
100.0%; Pred. No. 7.8e+05;
Indels 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= OTHER
/note= "(2R.6R)-2-amino-6,7-bis(SteO)-4-
thiaheptanoyl-,
where SteO = octadecanoyloxy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -amino-6,7-dihydroxy-4-thiaheptanoic acid; bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2-amino-6,7-dihydroxy-4-thiaheptanoic acid deriv.34
                                                                                                                                                                                                Disclosure; Page 62; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR59898 standard; peptide; 4 AA.
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93JP-0056185.
93JP-0181735.
             93WO-US09339.
                                      92US-0954813.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                         Artavanis-tsakonas S,
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 2; Conserva
                                                                                                                  WPI; 1994-135221/16.
                                                                                                                                                                                                                                                                                                                                                                       4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                (UYYA ) UNIV
             30-SEP-1993;
                                      30-SEP-1992;
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22-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR59898;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR59898
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; 0

Gaps

; 0

Search completed: February 11, 2003, 18:16:57 Job time : 8.26804 secs

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Sequence 8, Appl
Sequence 21, Appl
Sequence 28, Appl
Sequence 61, Appl
Sequence 61, Appl
Sequence 61, Appl
Sequence 103, Appl
Sequence 11, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 29, Appl
Sequence 61, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Appl
Sequence 59, Appl
Sequence 8, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                              February 11, 2003, 18:14:31; Search time 2.47423 Seconds (without alignments) 59.459 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                         /ogn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FOTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FOTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-139-68-59

US-08-131-8

PCT-US94-09143-21

US-07-906-349A-15

US-08-174-355A-28

US-08-174-355A-62

US-08-174-355A-105

US-08-174-355A-105

US-08-174-355A-105

US-08-174-355A-105

US-08-174-355A-105

US-08-174-355A-105

US-08-174-355A-105

US-07-872-673B-11

US-08-174-355A-105

US-07-969-305-59

US-07-969-305-61

US-07-969-305-81
                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                       262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                    Maximum Match 100%
Listing first 45 summaries
                                                     - protein search, using sw model
                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                              seq length: 0 seq length: 2000000000
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                                                                                                                              US-09-380-738A-5
13
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Match Length
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Maximum DB
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Appl Appl Appl Appl Appl Appl Appl Appl		0
		Gaps
Sednence Sed		0;
US-07-789-184-93 US-08-323-170B-3 US-08-475-263-82 US-08-475-263-82 US-08-475-263-93 US-08-485-886-93 US-08-485-886-93 US-08-485-886-93 US-08-485-886-93 US-08-485-886-93 US-08-408-604A-7 US-08-456-131-25 US-08-477-362-82 US-08-477-362-82 US-08-477-362-82 US-08-477-362-82 US-08-477-362-82 US-08-477-362-82	asan mains in FokI ndonuclease hman	re 10; DB 1; Length 3; ed. No. 2e+05; Mismatches 0; Indels
US-07-78 US-08-32 US-08-40 US-08-40 US-08-40 US-08-40 US-08-40 US-08-40 US-08-40 US-08-40 US-08-40 US-08-40 US-08-40	6564A riniv al Do ion E 81.0 #1.0 #1.0 83.41	Sco 9; Pr 0;
4444444444444	Lication US/08126 50 TION: handrasegaran, Sr handrasegaran, Sr NYION: Restriction UERNCES: 4 GO New York Ave., ington CO	76.9%; 100.0%; ative
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ILT 1 18-126-54A-21 quence 21, Application US/0812 quence 21, Application US/0812 quence 21, Application US/0812 TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TOTAL STREET: 1100 New YORK AVE. TOTAL TOT	76. imilarity 100 ; Conservative
000000000000000000000000000000000000000	ULT 1 08-126-564A-21 08-126-564A-21 adenance 21, Applica detent No. 5436150 GENERAL INFORMATION APPLICAMY: Chand TITLE OF INVENTIO TITLE OF INVENTIO UNDRER OF SEQUENC CORRESPONDENCE AD ADDRESSEE: U.S. STREEF: 1100 N. CITY: Washingt. STATE: D.C. COUNTRY: USA ZIP: 20005-391 COMPUTER READBLE MEDIUM TYPE: F COMPUTER READBLE MEDIUM TYPE: F COMPUTER READBLE SOFTWARE: PATE SOFTWARE: PATE SOFTWARE: PATE SOFTWARE: VOIN TELEDIOM TYPE: TILNO APTICATION NUM FILING DATE: Z. CLASSIFICATION NUM FILING DATE: Z. TELEPAX: 202-8: TELEPAX:	fatch scal S 2 2 1 EE 5 1 EE 5 1 EE 2
22 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT 1 US-08-126-5 Sequence Sequence TITLE TITLE TITLE TITLE TITLE COUNTY STRA SCOT SOF SOF SOF SOF SOF SOF SOF SOF SOF SOF	Query N Best Lo Matches Qy 4

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6714627 CUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Amino Acid
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STRANDEDNESS: Unl
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TOPOLOGY: Linear
US-08-539-432-8
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ZIP: 20005-3918
NEW YORK
NEW YORK
                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US94-09143-21
                                              COUNTRY:
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OTHER INFORMATION: /note = "Xaa is modified amino acid as
OTHER INFORMATION: described in specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
76.9%; Score 10; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                               US-08-174-365A-59
; Sequence 59, Application US/08174365A
; Patent No. 5478809
; GENERAL IMPORMATION:
APPLICANT: Selichi TANIDA et al.
TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: MEDABALIMI, JOHN L.
TITLE OF INVENTION: ELEMENT OF VIRAL
TITLE OF INVENTION: ELEMENT OF VIRAL
TITLE OF INVENTION: PROTEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCES: 19
CORRESPONDENCE ADDRESSE:
ADDRESSE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                 ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFFWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,365A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: December 28, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-539-432-8
; Sequence 8, Application US/08539432
; Patent No. 5872210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                           CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-174-365A-59
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                                              RESULT 2
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kokulis, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PNK/4130/82506/CLB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3503
TELEFRAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.9%; Score 10; DB 2; ilarity 100.0%; Pred. No. 2e+05; Conservative 0; Mismatches (
                                                                                                                                                                     FILING DATE: 05-OCT-1995
CLASSIFICATION: 514
ATTONNEY AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4194
TELECHONE: (212) 758-4800
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0,
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09143
FILING DATE: 23-AUG-1994
                                                                         OPERATING SICOL SOFTWARE: ASCII CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/539,432 TITING DATE: 05-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,564
FILING DATE: 27-SEPTEMBER-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application PC/TUS9409143 GENERAL INFORMATION:
                          COMPUTER: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
ZIP: 10054
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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Best Local Similarity
2; Conserve
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us-09-380-738a-5.rai

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OTHER INFORMATION: /note = "Xaa is modified amino acid as OTHER INFORMATION: described in specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.9%; Score 10; DB 1; Length 4; 100.0%; Pred. No. 2e+05; tive 0; Mismatches 0; Indels
                 GENERAL INFORMATION:

APPLICANT: Selichi TANIDA et al.

TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Selichi TANIDA et al. TITLE OF INVENTIONE: 4-THIAHEPTANOIC ACID DERIVATIVES NUMBER OF SEQUENCES: 106 CORRESPONDENCE ADDRESS:
                                                                                                              ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.5 inch, 144 mb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                      US/08/174,365A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-174-365A-61

Sequence 61, Application US/08174365A

Patent No. 5478809

GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                       December 28, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: modified site
                                                                                                                                                                     STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: December CLASSIFICATION: 514
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-174-365A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlik, Edward Y.
APPLICANT: Shoulik, Bediamin L.
TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
TITLE OF INVENTION: TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES AN
TITLE OF INVENTION: TARGET PROTEINS
                                                                                                                                                                                                        ö
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                                                                                                                                                                                                          Gaps
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0
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0
                                                                                                                                                                Score 10; DB 5; Length 3;
Pred. No. 2e+05;
                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 10; DB 1; Length 4;
Pred. No. 2e+05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/906,349A FILING DATE: 30-JUN-1992 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419 Seventh Street, N.W
                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/07906349A Patent No. 5434064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 28, Application US/08174365A
                                                                                                                                                76.9%; Sco.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NDBER: 07/643,237
FILLING DATE: 18-JAN-1991
TELECOMMUNICATION INFORMATION:
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                 SEQUENCE CHARACTERISTICS;
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                  LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Conservative
                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US94-09143-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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MOLECULE TYPE: peptide
                                                                                                                                                Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20004
                                                                                                                                                                                                                                                                                                                          RESULT 5
US-07-906-349A-15
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                                LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                    4 EE 5
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NAME/KEY: modified site
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LENGTH: 4 amino acids
                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 100.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: December CLASSIFICATION: 514
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                              single
                                                                                                                                                                                                            IDENTIFICATION METHOD:
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                                                                                          TYPE: amino acid
STRANDEDNESS: sir
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IRY: U.S.A.
20005
                                                                                                                                  TOPOLOGY: linear
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US-08-174-365A-67
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OTHER INFORMATION: /note = "Xaa is modified amino acid as
OTHER INFORMATION: described in specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.9%; Score 10; DB 1; Length 4; 100.0%; Pred. No. 2e+05; tive 0; Mismatches 0; Indels
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Patent No. 5478809
GENERAL INFORMATION:
APPLICANT: Selichi TANIDA et al.
TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,365A
FILING DATE: December 28, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                         US/08/174,365A
                                                                         December 28, 1993
                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                       61:
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
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Best Local Similarity 100.v
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                                                                                                                                                                                                                                                                                                                                                                          1: 4 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear
                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                CLASSIFICATION:
                                                                               FILING DATE:
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OTHER INFORMATION: /note = "Xaa is modified amino acid as
OTHER INFORMATION: described in specification"
CTHER INFORMATION: /note = "Xaa is modified amino acid as OTHER INFORMATION: described in specification" US-08-174-365A-62
                                                                                          76.9%; Score 10; DB 1; Length 4; 100.0%; Pred. No. 2e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Selichi TANIDA et al.
TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Wenderoth, Lind & Ponack
STREET: Wenderoth, Lind & Ponack
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,365A
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NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/CDCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
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               76.9%; Score 10; DB 1; Length 4;
100.0%; Pred. No. 2e+05;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.9%; Score 10; DB 1; Length 4; 100.0%; Pred. No. 2e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Schichi TANIDA et al.
TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/174,365A
FILING DATE: December 28, 1993
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; Sequence 105, Application US/08174365A
; Patent No. 5478809
; GENERAL INFORMATION:
                                                                                                                                                                                                                 ; Sequence 103, Application US/08174365A
; Patent No. 5478809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
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                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
Query Match
Best Local Similarity
'-hng 2; Conserve
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es 2; Conserv
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Patent No. 5523167

GENERAL INFORMATION:
APPLICANT: Lewis C. Cantley
APPLICANT: Zhou Song yang
TITLE OF INVENTION: Substrate Specificity of Protein Kinases
NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note = "Xaa is modified amino acid as OTHER INFORMATION: described in specification"
US-08-174-365A-105
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APPLICANT: Selichi TANIDA et al.
TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                               %E: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, suite 510
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                   US/08/174,365A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/174, FILING DATE: December 28, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                        SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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                                                                                            STREET: 805 ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 2; Conserv
                                                                                                                                            STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                  20005
                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.9%; Score 10; DB 1; Length 4; 100.0%; Pred. No. 2e+05; 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEE: IMMULOGIC PHARMACEUTICAL CORPORATION : One Kendall Square, Building 600 Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1
; OTHER INFORMATION: /note= "Xaa is phospho-Tyr"
US-08-178-570-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Channing, Stacey L. REGISTRATION NUMBER: 31,095
REFERENCE/DOCKET NUMBER: IPC-027/imi-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morvile, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
CORRESPONDENCE ADDRESS: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCIT TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,529A
FILING DATE: 19911213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                         US/08/178,570
                                                                                                                                                          BBI-004
                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: DECONTI, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-004
TELECOMMUNICATION INFORMATION:
TELEPRA: (617) 227-7400
TELEPRA: (617) 227-7400
TELEPRA: (617) 227-5941
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35, Application US/07807529A Patent No. 5547669
                                  APPLICATION NUMBER: US/08/17
FILING DATE: JANUARY 7, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rogers, Bruce L.
Morgenstern, Jay
Bond, Julian F.
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
SOFTWARE: ASCII text CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                             !: 4 amino acids
amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19911213
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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Best Local Similarity
Matches 2; Conserv
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APPLICANT: ROGERS
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APPLICANT:
                                                                                                                                                                                                                                                                           LENGTH:
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APPLICANT: Toshiya HAYANO, Setsuko KATO, No. 5578466uhiro TAKAHASHI, and Mass
TITLE OF INVENTION: Co-expression System of Protein Disulfide Isomerase Gene
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARPLICATION NUMBER: Japanese Patent Application No. 5578466. 114074/91 and FILING DATE: 18-APR-1991 and 30-OCT-1991
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD: ER retention of proteins having this signal OTHER INFORMATION: located at the C-terminus of mouse protein disulfide isc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUBLICATION INFORMATION:
AUTHORS: Mazzarella, R. A., Srinivasan, M., HaugeJorden and S. M. and Greer.
TITLE: ER972, an abundant luminal endoplasmic reticulum protein, contains t JOURNAL: 1 5 Biol. Chem.
VOLUME: 265
PAGES: 1094-1101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.9%; Score 10; DB 1; Length 4; 100.0%; Pred. No. 2e+05; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Type 2DD, 3.50 inch, 720 KB COMPUTER: Apple Macintosh SE OPERATING SYSTEM: Apple DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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FILTNO PARTY FILTNO PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PARTY BELLING PAR
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19920417
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MOLECULE TYPE:
DESCRIPTION: peptide
FRAGMENT TYPE: C-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/07872673B
Patent No. 5578466
GENERAL INFORMATION:
APPLICANT: TOSHLYA HAYANO, Setsukc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: ER retention signal
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 494-0060
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity luv..
                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-terminus
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                                                                                                                                                                                                                           TYPE: AMINO ACID TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMINO ACID
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LIY: BOSTON
STATE: MAC
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                                                                                                                                                                                                                                                                                                                                                           US-07-807-529A-35
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February 11, 2003, 18:19:51; Search time 2.42268 Seconds (without alignments) 52.729 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                   140259 seqs, 25548876 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
                                                                                                                                                                              US-09-380-738A-5
13
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                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                     Sequence:
                                                                                                                  Run on:
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/ cgn2_6/ptodata/2/pubpaa/USO6_NEW_Ton.p.pp;
/ cgn2_6/ptodata/2/pubpaa/USO6_NEW_Ton.p.pp;
/ cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep;
/ cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep;
/ cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep;
// cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep;
// cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep;
// cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep;
// cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep;
// cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep;
// cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep; /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 17. Anni	ά.		,,,	Sequence 51. Appl	Sequence 52. Appl	Sequence 56. Appl	Sequence 37. Appl	Segmence 37, April		, ,	, ,	, ,	1. A	ì -	+ <	, ,	seduence o, Appri	Sequence 6, Appli	Sequence 727, App	
ID	US-09-742-096-17	US-09-742-096-18	US-09-742-096-19	US-09-178-286-21	US-09-264-516A-51	US-09-264-516A-52	US-09-880-132-56	US-10-061-395-37	US-10-117-641-37	US-10-087-905-5	US-10-059-720-62	US-10-235-552-3	US-09-736-611-15	US-09-740-359-1	US-09-866-824A-1	US-09-866-824A-4	116-00-866-824A-F	C 44.30 000 C0 C0	US-09-866-824A-6	US-09-834-765-727	
DB		σ	σ	6	6	6	6	6	6	6	6	6	10	10	10	10	0	1 .	10	10	
& Query Match Length DB	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	• •	4	4	
% Query Match	76.9	6.97	6.97	76.9	76.9	76.9	76.9	76.9	6.97	76.9	76.9	6.94	6.97	6.97	76.9	76.9	76.9	100	6.0	76.9	
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Result No.	П	7	3	4	2	9	7	89	6	10	11	12	13	14	15	16	17	0	D C	19	

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Sequence 17, Application US/09742096

Batent No. US20020155441A1

GENERAL INFORMATION:

APPLICANT: DRUIGHE, PIERRE

TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES

FILE REFERENCE: 200773US0D1V

CURRENT APPLICATION NUMBER: US/09/742,096

FILE REFERENCE: 200773US0D1V

CURRENT FILING DATE: 1998-02-06

PRIOR APPLICATION NUMBER: WS 08/973,642

PRIOR APPLICATION NUMBER: FF 95/07007

PRIOR PAPLICATION NUMBER: FF 95/07007

PRIOR FILING DATE: 1996-06-13

PRIOR FILING DATE: 1995-06-13

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn version 3.1
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RESULT 1
US-09-742-096-17
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Best Local S
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US-09-264-516A-52
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APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 200773USGDIV
CURRENT FILING DATE: 2007-12-22
CURRENT FILING DATE: 2000-12-22
PRIOR PILING DATE: 1998-02-06
PRIOR FILING DATE: 1998-02-06
PRIOR FILING DATE: 1996-06-12
PRIOR FILING DATE: 1996-06-12
PRIOR FILING DATE: 1996-06-12
PRIOR FILING DATE: 1996-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PARCHINI VERSION 3.1
SEQ ID NO 19
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                        TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES FILE REFERENCE: 200773USODIV
CURRENT APPLICATION NUMBER: US 08/9742,096
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 08/973,642
PRIOR FILING DATE: 1998-02-06
PRIOR FILING DATE: 1998-06-13
PRIOR FILING DATE: 1995-06-13
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APPLICANT: Baird, Andrew
APPLICANT: Gonzalez, Ana Maria
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ORGANISM: Artificial Sequence
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DAUBERSIES, PIERRE
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Best Local Similarity
Matches 2; Conserv
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US-09-742-096-19
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US-09-178-286-21
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DELIVERY OF TITLE OF INVENTION: AGENTS FOR NEURONAL REGENERATION AND SURVIVAL: FILE REFERENCE: 760100 43333.
CURRENT APPLICATION NUMBER: US/09/178,286
CURRENT FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 4
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APPLICANT: Byers, Stephen
APPLICANT: Byers, Stephen
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING
TITLE OF INVENTION: CANCER METASTASIS
FILE REFERENCE: 100086.40723.08
FILE REFERENCE: 100086.40723.08
FRIOR PAPLICATION NUMBER: 09/234,395
PRIOR APPLICATION NUMBER: 09/234,395
PRIOR APPLICATION NUMBER: 09/214,395
PRIOR APPLICATION NUMBER: 09/073,040
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 319
SOFTWARE: FastsEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Synthetic Peptide - example CTHER INFORMATION: cytoplasm-translocation signal sequence US-09-178-286-21
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Best Local Similarity 100.0
Matches 2; Conservative
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Sequence 56, Application US/09880132

Sequence 56, Application US/09880132

Sequence 56, Application US/09880132

Sequence 56, Application US/09880132

SEQUENCE TO THE PROPERTY SEQUENCE TO THE PROPERTY SEQUENCE TO THE PROPERTY SEQUENCE TO THE PROPERTY SEQUENCE TO THE PROPERTY SEQUENCE TO THE PROPERTY SEQUENCE TO THE PRIOR PLILING DATE: 1999-09-28

PRIOR PLILING DATE: 1999-02-28

PRIOR PLILING DATE: 1999-02-12

PRIOR FILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 67

SEQ ID NO 56
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FOUR THORMATION: Synthesized peptide with an OB-cadherin cell
CTHER INFORMATION: adhesion recognition sequence
US-09-264-516A-52
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7 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING
7 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING
7 TITLE OF INVENTION: COANCER METASTASIS
7 FILE REFERENCE: 100086.407C3
7 CURRENT APPLICATION NUMBER: US/09/264,516A
7 CURRENT FILING DATE: 1999-01-20
7 PRIOR APPLICATION NUMBER: 09/234,395
7 PRIOR APPLICATION NUMBER: 09/187,859
7 PRIOR PILING DATE: 1999-01-20
7 PRIOR PILING DATE: 1999-01-20
7 PRIOR FILING DATE: 1999-05-05
7 NUMBER OF SEQ ID NOS: 319
7 SOFTWARE: FESTEEQ FOR WINGOWS VEFSION 3.0
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Matches 2; Conservative
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US-10-061-395-37
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Sequence 37, Application US/10117641
Publication No. US20020194640A1
GENERAL INFORMATION:
APPLICANT: Misra, Santosh et al.
TITLE OF INVENTION: DIANT PROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AN TITLE OF INVENTION: ITS USE
FILE REFERENCE: 62586
CURRENT APPLICATION NUMBER: US/10/117,641
CURRENT FILING DATE: 2002-04-03
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Heterologous signal sequence for the endoplasmic reticulum US-10-061-395-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haaland, Perry D.
APPLICANT: Sherman, Douglas B.
APPLICANT: Stewart II, Walter W.
APPLICANT: Lloyd, Sheila A.
APPLICANT: Campbell, Robert L.
TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR TITLE OF INVENTION: FORMULATING CULTURE MEDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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TITLE OF INVENTION: Methods of Identifying Regulator Molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.9%; Score 10; DB 9; Length 4; 100.0%; Pred. No. 1.2e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                 FILE REFERENCE: 1821.0080003
CURRENT APPLICATION NUMBER: US/10/061,395
CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/265,880
PRIOR FILING DATE: 2001-02-27
PRIOR FILING DATE: 2001-02-65
PRIOR FILING DATE: 2001-02-65
PRIOR FILING DATE: 2001-02-65
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: P3250
CURRENT APPLICATION NUMBER: US/10/087,905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/10087905
Publication No. US20030022152A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Pseudotsuga menziesii
                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.v
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Best Local Similarity
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KRYLOV, DMILTY
TITLE OF INVENTION: EXTENSION OF A PROFEIN-PROTEIN
INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: hypothetical is-10-087-905-5
                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                           Length 4;
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7. 1.2e+05;
0;
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NAME: Serunian, Leellie A.
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4199US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/059,720
FILING DATE: 29-Jan-2002
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/01,654
FILING DATE: 31-JUL-1995
APPLICATION NUMBER: 60/018,496
FILING DATE: 29-MAY-1996
APPLICATION NUMBER: 08/690,011
FILING DATE: 31-JULY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                      Query Match 76.9%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 1.2 Matches 2; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELLULAR PROTEIN NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-10-059-720-62
CURRENT FILING DATE: 2002-03-05
PRIOR PAPLICATION NUMBER: US/09/359,260
PRIOR FILING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 5
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-059-720-62; Sequence 62, Application US/10059720; Publication No. US20030027314A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VINSON, Charles R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4 amino acids
                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-235-552-3

US-10-235-552-3

Sequence 3, Application US/10235552

Sequence 3, Application US/10235552

Publication No. US20030027768A1

GENERAL INFORMATION:
APPLICANT: Mazar, Andrew P.
APPLICANT: JOHGS, Terence L.
TITLE OF INVENTION: ANTI-INVASIVE AND ANTI-ANGIOGENIC COMPOSITIONS AND METHODS
FILE REFERENCE: 38369-18365
CURRENT APPLICATION NUMBER: US/10/235,552

CURRENT FILING DATE: 1997-09-06

PRIOR FILING DATE: 1997-07-25

NUMBER OF SEQ ID NOS: 9

SEQ ID NO 3

LENGTH: 4
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                                                                    Gaps
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OTHER INFORMATION: Description of Artificial Sequence: substitution,
OTHER INFORMATION: deletion or addition variants of SEQ ID NO:2
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: UNSURE:
LOCATION: (1)
COTHER INFORMATION: amino acid to which is bound an amino terminal
OTHER INFORMATION: group; X attached to Pro is a peptidomimetic
COTHER INFORMATION: compound
US-10-235-552-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/09736611
; Betent No. US20010023069A1
; Patent No. US20010023069A1
; GENERAL INFORMATION:
    APPLICANT: Kelarsholm: Type Application Syend
    APPLICANT: Ludvigsen, Thomas
; APPLICANT: Kaarsholm, Niels
; TITLE OF INVENTION: Method For Making Insulin Precursor and
; TITLE OF INVENTION: Method For Making Insulin Precursor Analogs
; TITLE OF INVENTION: MOBBER: US/09/736,611
; CURRENT APPLICATION NUMBER: 60/181,443
; PRIOR FILING DATE: 2000-02-10
; PRIOR PILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PA 1999 01868
; PRIOR APPLICATION NUMBER: PA 1999 01868
; PRIOR APPLICATION NUMBER: PA 2000 00440
; PRIOR PILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 18
; NUMBER OF SEQ ID NOS: 18
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                     Length 4;
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                76.9%; Score 10; DB 9; Le
ilarity 100.0%; Pred. No. 1.2e+05;
Conservative 0; Mismatches 0;
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FastSEQ for Windows Version 4.0
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Query Match
Best Local Similarity
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Best Local Similarity
Matches 2; Conserv
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US-09-736-611-15
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SEQ ID NO 15
LENGTH: 4
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Sequence 1, Application US/09740359

Patent No. US20010041787A1

GENERAL INFORMATION:

APPLICANT: Kieldsen, Thomas Borglum

APPLICANT: Ludvigsen, Svend

TITLE OF INVENTION: Method for making insulin precursors and

TITLE OF INVENTION: Insulin precursor analogues having improved fermentation

TITLE OF INVENTION: 1 insulin precursor analogues having improved fermentation

TITLE OF INVENTION: 1 insulin precursor analogues having improved fermentation

TITLE OF INVENTION: 1 insulin precursor analogues having improved fermentation

FILE REFERENCE: 6448.2000-15

CURRENT FILING DATE: 2000-12-19

PRIOR PAPLICATION NUMBER: PA 2000 00443

PRIOR FILING DATE: 2000-03-17

PRIOR PAPLICATION NUMBER: 60/211,081

PRIOR FILING DATE: 2000-06-13

PRIOR PAPLICATION NUMBER: 60/181,450

PRIOR PAPLICATION NUMBER: 60/181,450

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FASLSEQ for Windows Version 4.0
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                                                                                              76.9%; Score 10; DB 10; Length 4; 100.0%; Pred. No. 1.2e+05; tive 0; Mismatches 0; Indels
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US-09-866-824A-1
; Sequence 1, Application US/09866824A
; Patent No. US20020035243A1
; GENERAL INFORMATION:
; APPLICANT: Infeld, Dominik
; APPLICANT: Ludin, Christian
; APPLICANT: Schreder, Thomas
; TILLE OF INVENTION: Transport System Conjugates
; FILE REFERENCE: 3006-039
; CURRENT FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 1
; LEGTHEL APPLICATION VERSION 3.0
; SEQ ID NO 1
; LEGTHEL APPLICATION VERSION 3.0
; SEQ ID NO 1
; LEGTHEL APPLICATION VERSION 3.0
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                            ; ORGANISM: N-terminal extension US-09-736-611-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                 Conservative
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; ORGANISM: Mini C-peptide
US-09-740-359-1
                                                                                              Ouery Match
Best Local Similarity
Matches 2; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 2; Conserv
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; TYPE: PRT
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February 11, 2003, 18:17:01 ; Search time 34.3299 Seconds (without alignments) 93.903 Million cell updates/sec
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                    Compugen Ltd.
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compuc
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                                                                                                                                                                                                                                                                                              4569144 seqs, 644733110 residues
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Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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13
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                                                                                                                                                                   Title:
Perfect score:
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Maximum DB
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                                                                                                   Run on:
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/cgn2_6/ptodata/1/paa/US100_COMB.pep:*/cgn2_6/ptodata/1/paa/US101_COMB.pep:* /cgn2_6/ptodata/1/paa/US099_COMB.pep:* 'ptodata/1/paa/US102_COMB.pep:* /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 303, App Sequence 21, Appl Sequence 11, Appl Sequence 69, Appl Sequence 66, Appl Sequence 11, Appl
SUMMARIES ID	PCT-USO1-01786A-303 US-08-017-493-21 US-09-692-077B-11 US-09-920-306-59 US-09-920-306-66 US-10-001-073-11
DB	200 203 203 203
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a Query Match	76.9 76.9 76.9 76.9 76.9
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USOD -31721- USO2 -02814- USO3 -10999- USO3 -10999- USO3 -10999- USO3 -10999- USO3 -10999- USO3 -10999- USO3 -10999- USO3 -10868- USO3 -10868- USO3 -10868- USO3 -10868- USO3 -10809- USO3	-08 - 38 -08 - 38 -08 - 43 -08 - 43
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ALIGNMENTS

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                                                                       APPLICANT: SMITHKLINE BEECHAM CORPORATION
TELE OF INVENTION: METHODS AND REAGENTS FOR PERFORMING
TITLE OF INVENTION: METHODS AND REAGENTS FOR PERFORMING
TITLE OF INVENTION: METHODS AND REAGENTS FOR PERFORMING
TITLE OF INVENTION: MUTHOROBIAL COMPOUND SCREENING
FILE REFERENCE: GMS0067
CURRENT APPLICATION NUMBER: PCT/US01/01786A
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/176,870
PRIOR APPLICATION NUMBER: 60/176,870
NUMBER OF SEQ ID NOS: 403
SOFFWARE: FASTSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.9%; Score 10; DB 1; Length 3; 100.0%; Pred. No. 4.2e+06; Live 0; Mismatches 0; Indels
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                           ; Sequence 303, Application PC/TUS0101786A ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Escherichia coli
PCT-US01-01786A-303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
'-haq 2; Conserva
PCT-US01-01786A-303
                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 303
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us-09-380-738a-5.rapm

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Sequence 59, Application US/09920306
; GENERAL INFORMATION:
; APPLICANT: Unilever PLC
; APPLICANT: Unilever NV
; TITLE OF INVENTION: Hormonal Analytes
; TITLE OF INVENTION: Hormonal Analytes
; TITLE OF INVENTION: Hormonal Analytes
; CURRENT APPLICATION WUMBER: US/09/920,306
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: EP00306613.1
; PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic CTHER INFORMATION: Peptide US-09-920-306-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.9%; Score 10; DB 23; Length 3; Best Local Similarity 100.0%; Pred. No. 4.2e+06; Matches 2; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 59
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                                                                                            US-09-920-306-59
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1 EE 2
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GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
TITLE OF INVENTION: Alpha-2B-adrenergic receptor polymorphisms
FILE REFERENCE: Sequences 1-22
CURRENT APPLICATION NUMBER: US/09/692,077B
CURRENT FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Endonuclease
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, Darby & Cushman
STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.9%; Score 10; DB 20; Length 3; 100.0%; Pred. No. 4.2e+06; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CAPLICATION NUMBER: US/08/017,493
FILING DATE: 19930212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: KOKALIS. Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PNK/4130/97635/CLB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3503
TELEPRAK: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Releasen #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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Matches 2; Conservative
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MOLECULE TYPE: peptide
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ZIP: 20005-3918
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 2; Conserv
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CLASSIFICATION:
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                                            US-08-017-493-21
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CITY: Wa
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APPLICANT: Unilever PLC
APPLICANT: Unilever NV
TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for TITLE OF INVENTION: Hormonal Analytes
FILE REFERENCE: Peptide Mimotopes
CURRENT APPLICATION NUMBER: US/09/920,306
CURRENT APPLICATION NUMBER: US/09/920,306
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2000-08-03
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: peptide US-09-920-306-66
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GEBREAL INFORMATION:
APPLICANT: MURSHY, JOHN R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATMENT OF DISEASE
CURRENT SPELICANTION NUMBER: PCT/US00/31721
CURRENT PELLIG DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
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              APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REPERBNCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Haaland, Perry D.
APPLICANT: Sherman, Douglas
APPLICANT: Stewart, William
APPLICANT: Stewart, William
APPLICANT: Lioyd, Sheila A.
APPLICANT: Erickson, Bruce W. (deceased)
TITLE OF INVENTION: Peptides for Use in Culture Media
FILE REFERENCE: Peptides for Culture Media
CURRENT APPLICATION NUMBER: PCT/US01/17943
CURRENT APPLICATION NOWHER: PCT/US01/17943
NUMBER OF SEO ID NOS: 94
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: phospho-tyrosine
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: phospho-tyrosine-containing peptide
                                                                                                                                                                                                                                                                                                                            Query Match 76.9%; Score 10; DB 24; L. Best Local Similarity 100.0%; Pred. No. 4.2e+06; Matches 2; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-073-11
GENERAL INFORMATION:
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; OTHER INFORMATION: Heterologous signal sequence for the endoplasmic reticulum PCT-US02-02814-37
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APPLICANT: University of Rochester
APPLICANT: Sauderer, Maurice (U.S. Only)
APPLICANT: Sauth. Ernest S. (U.S. Only)
TITLE OF INVENTION: Methods of Identifying Regulator Molecules
FILE REFERENCE: 1821.0080003
CURRENT APPLICATION NUMBER: 60/271, 423
PRIOR APPLICATION NUMBER: 60/271, 423
PRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Version 3.1
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                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic; OTHER INFORMATION: peptide linker PCT-US01-17943-94
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Query Match

T6.9%; Score 10; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels
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APPLICANT: Hoffmann, Heidi M.
APPLICANT: Actuass, Reason and APPLICANT: Valenzuela, Dario B.
APPLICANT: Saini, Kulvinder Singh
TITLE OF INVENTION: Cell Adhesion-Mediating Proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Polynuclectides Encoding Them FILE REFERENCE: 1966.1014002
CURRENT APPLICATION NUMBER: PCT/US02/14457
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/289,179
PRIOR FILING DATE: 2001-05-07
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CT-10802-02814-37
Sequence 37, Application PC/TUS0202814
GENERAL INFORMATION:
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                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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SEQ ID NO 94
LENGTH: 4
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PCT-US97-04635-22
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                                                PCT-US93-10999-29
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                                RESULT 12
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APPLICANT: McDonnell, James M.
APPLICANT: Korngold, Robert
TITLE OF INVENTION: Compounds That Inhibit T Cell Proliferation And
TITLE OF INVENTION: Methods Using The Same
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
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                                                                                                                                                                                                   76.9%; Score 10; DB 1; Length 4; 100.0%; Pred. No. 4.2e+06; Live 0; Mismatches 0; Indels
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PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076,092
FILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,692
FILING DATE: 13-NOV-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TJU-904
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application PC/TUS9310999 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WORDPERFECT 5.1
                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                               ; OTHER INFORMATION: SH2 domain PCT-US02-14457-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS
                                                                                                                                                                                                                                              Conservative
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MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PS/2
OPERATING SYSTEM: I
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Best Local Similarity
Thes 2; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
PCT-US93-10999-27
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19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
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                                                                                                                                       FEATURE:
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TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS COMPRISING
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS PROTEINS AND/OR PEPTIDES AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 24
                                APPLICANT: Mameson, Bradford A. APPLICANT: Mobonnell, James M. APPLICANT: Mobonnell, James M. APPLICANT: Morpounell, James M. APPLICANT: Morpounell, Robert TITLE OF INVENTION: Compounds That Inhibit T Cell Proliferation And TITLE OF INVENTION: Methods Using The Same NUMBER OF SEQUENCES: 66 CORRESPONDENCES: 66 CORRESPONDENCE ADDRESSS: ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & Norris STREET: One Liberty Place - 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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APPLICANT: POTEMPA, JAN.
APPLICANT: TRAVIS, JAMES
APPLICANT: TRAVIS, JAMES
APPLICANT: GENCO, CAROLINE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10; DB 1; Length 4; pred. No. 4.2e+06;
                                                                                                                                                                                                                                                                                                                                                                            DISKETTE, 3.5 INCH, 1.44 Mb Storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 22, Application PC/TUS9704635 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: DeLuca, Mark
REGIGSTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-904
TELECOMMUNICATION INFORMATION:
Sequence 29, Application PC/TUS9310999 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/977,692
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/076,092
FILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
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TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                             ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PS/2
OPERATING SYSTEM: F
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PCT-US93-10999-29
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CLASSIFICATION:
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PCT-US97-12652-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39, Application PC/TUS9712618
GENERAL INFORMATION:
APPLICANT: University of Utah Reseearch Foundation
APPLICANT: Orgonetix, Inc.
TITLE OF INVENTION: Conantokins
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: D.C.
                                               ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/04635
FILING DATE: 21-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PCFF1 - COMPATIBLE COMPATIBLE SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATE: PCT/US97/12618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 08/684,742
FILING DATE: 22-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24,950
                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,945
FILING DATE: 22-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 103-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 488-8089
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS: single
not relevant
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
PCT-US97-04635-22
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Boulder
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                                   COUNTRY:
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                                                                                                                                                                                                                                                                               Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                        Query Match 76.9%; Score 10; DB 1; LA Best Local Similarity 100.0%; Pred. No. 4.2e+06; Matches 2; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.9%; Score 10; DB 1; La Best Local Similarity 100.0%; Pred. No. 4.2e+06; Matches 2; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JUREAL ARCHIVES.

APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Use of Conantokins
willings of SEOUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/12652
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/684,750
FILING DATE: 22-UUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/762,377
FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39, Application PC/TUS9712652 GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4800
TELEFAX: 202-962-9300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957 REFERENCE/DOCKET NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4800
                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
                                                                                                            4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-962-8300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202-502-8300
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                                                                                                        LENGTH: 4 amino a TYPE: amino acid STRANDEDNESS:
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CLASSIFICATION:
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                                                                                                                                                                                                                                 PCT-US97-12618-39
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2 EE 3

Search completed: February 11, 2003, 18:33:26 Job time : 35.3299 secs

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February 11, 2003, 18:17:56 ; Search time 5.72165 Seconds (without alignments) 72.734 Million cell updates/sec
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                            420401 seqs, 83231269 residues
                                                                                       OM protein - protein search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 15, Appl	77	72,	. 00	45	Sequence 47, Appl	16,	28	715	721,	15, 7	K	0	l C	56,	66	721.	90,	138,	13. 7	57,	62.	50.	, m	65,	17,
SUMMARIES	ID	US-10-275-360-15	PCT-US02-32007-57	PCT-US02-00667A-72	US-09-783-130A-8	US-09-611-257A-45	US-09-611-257A-47	US-09-856-886B-16	US-09-165-062A-28	US-09-799-250A-715	US-10-062-109A-721	US-10-316-421-15	US-10-191-254C-3	US-10-099-408A-10	US-10-176-791A-21	US-10-345-281-56	US-10-319-003-99	US-10-005-480A-721	PCT-US01-32150-90	US-09-653-812B-138	US-09-992-124B-13	US-09-992-124B-57	US-09-992-124B-62	US-09-800-770-50	US-09-800-770-53	US-09-636-243B-65	US-09-856-886B-17
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dР	Query Match	6.97	•						76.9	6.97	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	6.92	76.9	6.97	76.9	6.92	76.9
	Score	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
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25, Appl 26, 26, Appl 215, Appl 211, Appl 217, Appl 210, Appl 210, Appl 21,	РАТН	Gaps	ж
			GROWTH
Sednence Sed	HES	0	
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	BIOSYNTHESIS	a)	F C ₄
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US-09-856-886B-25 US-09-856-886B-25 US-10-281-652-15 US-10-213-512-31 US-10-213-512-31 US-10-313-003-100 US-10-35-20B-20 US-10-35-20B-20 US-10-35-20B-20 US-09-65-086-5 US-09-65-086-5 US-09-749-959-1 US-09-776-26BA-5 US-09-774-925A-70 US-09-794-925A-70 US-09-794-925A-70 US-09-794-925A-70 US-09-794-925A-70	LIGNMENTS 0 -DESOXX-D-XXLULOSE 275,360 /04537 88.9	DB 6; L43.5e+05;	
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		TYPE: PRT ORGANISM: S-10-2736- Query Match Best Local S Matches 2 4 EE 5 7 1 1	PCT-USO2-32007-57 Sequence 57, Application PC/TUSO232007 GENERAL INFORMATION: APPLICANN: Yale University TITLE OF INVERTION: NOGO RECEPTOR-MEDIATED BL FILE REFERENCE: C077 CIP PCT CURRENT APPLICATION NUMBER: PCT/USO2/32007 CURRENT PILING DATE: 2002-10-04 PRIOR PELLING DATE: 2001-10-06 NUMBER OF SEQ ID NOS: 57 NUMBER OF SEQ ID NOS: 57 LENGTH: 4 SEQ ID NO 57 LENGTH: 4 TYPE: PRT COGANISM: Attificial Sequence FRATURE: COTHER INFORMATION: Description of Artificial
2	LLT 1 0-275- 0-275- 0-275- 0-275- ILLE 0 ILLE CO ILLE RENTE OURRENT URRENT URRENT F RIOR F RIOR F RIOR F RIOR F OFTWAR 0 ID N	YPE: RGAN -275 -275 ry M t Lo ches	r 2 202- 202- 202- 202- 202- 208- 208- 208
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US-09-611-257A-47
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: CLOOld48
CURRENT FILING DATE: 2001-02-15
PRIOR PRIOR APPLICATION NUMBER: 60/256,354
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 4
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Sequence 72, Application PC/TUS0200667A
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF MARYLAND, COLLEGE PARK
TITLE OF INVENTION: METHODS FOR DETERMINING RING NUMBER IN CAROTENOIDS BY
TITLE OF INVENTION: LYCOPENE EPSILON - CYCLASES AND USES THEREOF
FILE REFERENCE: 108172-00055
CURRENT APPLICATION NUMBER: PC7/US02/00667A
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: 60/261,473
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 72
FENOME.
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                                                           76.9%; Score 10; DB
ilarity 100.0%; Pred. No. 3.5
Conservative 0; Mismatches
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GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion
APPLICANT: et al.
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; OTHER INFORMATION: peptide PCT-US02-32007-57
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Matches 2; Conserv
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Matches 2; Conserv
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US-09-783-130A-8
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Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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APPLICANT: Ballie, David L.
TITLE OF INVENTION: MAMMALLIAN T-TYPE CALCIUM CHANNELS
TITLE OF INVENTION: MAMMALLIAN T-TYPE CALCIUM CHANNELS
FILE REFERENCE: 38109-20007, 21
CURRENT PELLICATION NUMBER: US/09/611,257A
CURRENT FILING DATE: 2000-07-06
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 47
LENGTH: 4
                                                                                 APPLICANT: Baillie, David L.
TITLE OF INVENTION: MAMMALIAN T-TYPE CALCIUM CHANNELS
FILE REPERENCE: 38109-20007.21
CURRENT ABLICATION NUMBER: US/09/611,257A
CURRENT FILING DATE: 2000-07-06
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PRIOR APPLICATION NUMBER: 09/346,794
PRIOR FILING DATE: 1999-07-02
PRIOR PELING DATE: 1999-07-02
PRIOR PELING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/039,204
PRIOR FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FASTEED for Windows Version 4.0
SEQ ID NO 45
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Sequence 45, Application US/09611257A GENERAL INFORMATION:
APPLICANT: Snutch, Terrance
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Matches 2; Conserv
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ORGANISM: Unknown
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US-10-062-109A-721
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US-10-316-421-15
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APPLICANT:
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               Sequence 16, Application US/09856886B
SEGNERAL INFORMATION:
APPLICANT: Bianchi, Elisabetta
APPLICANT: Ingallinelia, Paolo
APPLICANT: Ingallinelia, Paolo
APPLICANT: Pessi, Antonello
TITLE OF INVENTION: PHARMACEUTICAL COMPOUNDS FOR THE
TITLE OF INVENTION: INHIBITION OF HEPATITIS C VIRUS NS3 PROTEASE
TITLE REPRENCE: TYO13P BITTON OF HEPATITIS C VIRUS NS3 PROTEASE
CURRENT APPLICATION NUMBER: US/09/856,886B
CURRENT FILING DATE: 2001-07-26
PRIOR FILING DATE: 1999-11-24
PRIOR FILING DATE: 1998-11-26
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSEQ for Windows Version 4.0
SSC ID 0 16
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APPLICANT: LECY, SIMA
APPLICANT: SCHLESSINGER, JOSEPH
TILE OF INVENTION: PYCZ PRELATED PRODUCTS AND METHODS
FILE REFERENCE: 038602/0116
CURRENT APPLICATION NUMBER: US/09/165,062A
CURRENT APPLICATION NUMBER: 08/460,626
PRIOR APPLICATION NUMBER: 08/460,626
PRIOR APPLICATION NUMBER: 08/357,642
PRIOR FILING DATE: 1995-06-02
PRIOR FILING DATE: 1994-12-15
NUMBER OF SEQ ID NOS: 32
SOSTWARE: PATENTIN VOIC: 2.1
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US-09-165-062A-28
; Sequence 28, Application US/09165062A
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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Matches 2; Conservative
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US-09-856-886B-16
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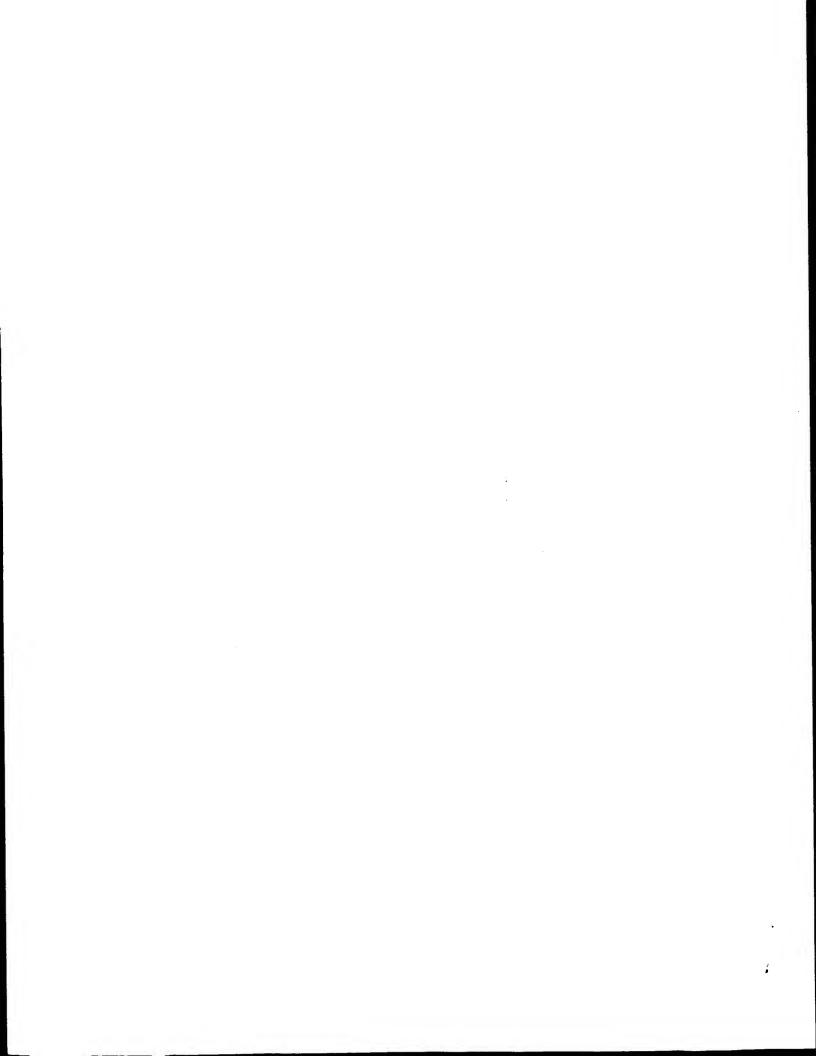
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APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: JANGDOVILE, Aya
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20062.01
CURRENT APPLICATION NUMBER: US/10/062,109A
PRIOR PILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARRE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Pia M. Challita-Eid
APPLICANT: Pia M. Challita-Eid
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Aya Jakobovits
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 1121PIFT: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129.34 usol (5118-20034.00)
CURRENT APPLICATION NUMBER: US/09/799,250A
CURRENT FAPLICATION NUMBER: US/09/799,250A
NUMBER OF SEQ ID NOS: 720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.9%; Score 10; DB 5; Length 4; 100.0%; Pred. No. 3.5e+05; Live 0; Mismatches 0; Indels
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APPLICAMT: Kjeldsen, Thomas
APPLICAMT: Ludvigsen, Svend
APPLICANT: Kaarsholm, Niels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Challita-Eid, Pia M.
Raitano, Arthur B.
Faris, Mary
Hubert, Rene S.
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Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-10-062-109A-721
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us-09-380-738a-5.rapn

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1 EE 2
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TITLE OF INVENTION: Method For Making Insulin Precursors and FITLE OF INVENTION: Insulin Precursor Analogs FILE CRINGENION: Insulin Precursor Analogs FILE CRINGENION: 1050-00-05; CURRENT APPLICATION NUMBER: US/10/316,421
CURRENT FILING DATE: 2002-12-11
PRIOR APPLICATION NUMBER: US/09/736,611
PRIOR FILING DATE: 2000-02-10
PRIOR PILING DATE: 2000-02-10
PRIOR PILING DATE: 2000-02-10
PRIOR PLING DATE: 2000-06-13
PRIOR PLING DATE: 2000-06-13
PRIOR PLING DATE: 2000-06-13
PRIOR PLING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
NUMBER OF SDD IN NOWHER: PA 2000 00440
SPRIOR FILING DATE: 2000-03-17
SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 10, Application:
    APPLICANT: D'Lima, Darryl
    APPLICANT: Lotz, Martin
    APPLICANT: Colwell, Clifford
    TITLE OF INVENTION: Process of Inhibiting Cell Death in
    TITLE OF INVENTION: Injured Cartilage
    FILE REFERENCE: TSRI 801.1/NOV 0237P
    CURRENT APPLICATION NUMBER: US/10/099,408A
    CURRENT FILING DATE: 2002-12-10
    PRIOR APPLICATION NUMBER: 60/276,183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wyeth
TITLE OF INVENTION: CASPASE 9 ACTIVATION AND USES THEREFOR
FILE REFERENCE: AM101006
CURRENT APPLICATION NUMBER: US/10/191,254C
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.9%; Score 10; DB 6; Length 4; llarity 100.0%; Pred. No. 3.5e+05; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Substrate US-10-191-254C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial
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Matches 2; Conserv
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US-10-099-408A-10
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                                                                                                                                                                                                                                                  NAME/KEY: MOD_RES
LOCATION: 1
OTHER INFORMATION: Carbobenzyloxy protection of the N-terminal amino
OTHER INFORMATION: group
                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Methyl ester protection of the carboxylic acid
OTHER INFORMATION: side chain;
OTHER INFORMATION: C-terminal fluoromethyl ketone where the C-1
OTHER INFORMATION: carbon of the aspartyl residue is the carbonyl
COTHER INFORMATION: carbon of the ketone
                                                                                                                                                                        caspase inhibitor; fluoromethyl ketone on the C-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Basolateral Sorting Signal and TITLE OF INVENTION: Inhibitors Thereof FILE REPRENCE: 50275/002001
CURRENT APPLICATION NUMBER: US/10/176,791A
CURRENT FILING DATE: 2002-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Cluster of Charged Amino-Acids US-10-176-791A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUKKENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: PCT/EP00/13141
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/CH99/00624
PRIOR PILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 76
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
                   NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BERNHARD M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 21, Application US/10176791A
; GENERAL INFORMATION:
; APPLICANT: WEHRLE-HALLER, BERNHARD M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-10-345-281-56
Sequence 56, Application US/10345281
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2001-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                               OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MOD_RES
LOCATION: 4
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Search completed: February 11, 2003, 18:35:22 Job time : 6.72165 secs



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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 11, 2003, 18:14:11 ; Search time 4.38144 Seconds Run on:

(without alignments)
109.706 Million cell updates/sec

US-09-380-738A-5 Perfect score: Title:

1 XXXEE 5 Sequence:

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

PIR_73:* Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

alpha-myosin heavy calsequestrin, fas Na+-transporting A pallidipin - assas traM protein - Esc hydrogensulfite re tocopherol-binding aspartate kinase (ferredoxin a2 - Ja caldesmon - rabbit calsequestrin, car fibrinogen beta ch fibrinogen beta ch seed storage prote cytochrome-c oxida photosystem I 17.5 - domestic late G1-69 protein cytochrome-c oxida calpain (EC 3.4.22 LuxC protein - Pho T-cell receptor be cytochrome-c oxida 6-phosphofructokin complement C3b rec chemical-sense-rel hypothetical 1.5K hypothetical 1.5K tetracenomycin A2 Description gastrin SUMMARIES A32014 S11556 I46868 B39040 S45648 \$29272 B47594 \$69165 A44873 A61230 C24180 D24180 PH0108 PH0942 S65388 S39392 B39853 A55149 JQ2307 S55238 C38925 S43625 DB Query Match Length Score Result NO.

microtubule-associ	hypothetical profe	aminotransferase	myosin heavy chain	hypothetical proto	sood stored prote	beta-conglucinin a	hemocyanin chain s	chondroitin sulfat	To heavy chain CDR	major urinary prot	Na+/K+-exchanging	Na+/K+-exchanging	aminotransforasco	tubulia hata ahai	cubulin beta chain	protein QA300045 -
S09349	S41909	PC2124	A39233	T46794	A38925	516335	F61308	B47171	PT0228	S68271	S27024	S27023	PC2122	539713	0.00 kg	FAUUSI
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10	10	10	10	1(7	-	_	_		П		П		_	-	Á

ALIGNMENTS

RESULT 1 S55238 pallidipin - assassin bug (fragment) C;Species: Triatoma pallidipennis (assassin bug) C;Date: 19 Mar-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000 C;Accession: S55238	gment) nis (assassin bug) _revision 18-Jul-1997 #text_change 19-May-2000
R;Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Sch Biochem. J. 307, 465-470, 1995	Deske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Sch
A;Title: Expression of active recombinant pallidipin, a novel platelet aggregation A;Reference number: S55238; MUID:95251610; PMID:7733884 A;Accession: S55238	recombinant pallidipin, a novel platelet aggregation JID:95251610; PMID:7733884
A;Molecule type: protein A;Residues: 1-4 <hae></hae>	
Query Match 76.9%; Score 10; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels	<pre>%; Score 10; DB 2; Length 4; 0%; Pred. No. 2.8e+05; 0; Mismatches 0; Indels 0; Gaps 0;</pre>

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tram protein - Escherichia coli plasmid R100 (fragment)

Cispecies: Escherichia coli plasmid KlUU (Iragment)
Cispecies: Escherichia coli
Cispecies: Escherichia coli
Cispecies: Escherichia coli
Cispecies: Allan-1989 #sequence_revision 22-Jun-1989 #text_change 16-Feb-1997
Ciscoession: A32014
J. Bacteriol. 170, 2749-2757, 1988
A;Title: Identification and characterization of the products from the traJ and tra'
A;Reference number: A32014; MUID:88227859; PMID:2836369
A;Accession: A32014
A;Status: preliminary
A;Accession: Lype: DNA
A;Residues: 1-5 < INA>
C;Genetics:

A; Genome: plasmid C; Keywords: DNA binding

h 76.9%; Score 10; DB 2; Length 5; Similarity 100.0%; Pred. No. 2.8e+05; 2; Conservative 0; Mismatches 0; Indels Best_Local Similarity Matches 2; Conserv Query Match

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Gaps

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EE 5 4 EE 5 δ

n RESULT 3 Length 7;

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$45648

Na+-transporting ATP synthase (EC 3.6.1.-) alpha chain - Acetobacterium woodii (fransporting ATP synthase alpha chain

C;Species: Acetobacterium woodii

C;Species: Acetobacterium woodii

C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999

C;Accession: $45648

R;Reidinger, J.; Mueller, V.

Eur. J. Biochem. 223, 275-283, 1994

A;Title: Purification of ATP synthase from Acetobacterium woodii and identification
A;Reference number: $45648; MUID:94307271; PMID:8033902
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.9%; Score 10; DB 2; Le Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-3;4-7 <REI>
A;Experimental source: DSM 1030
C;Keywords: hydrolase
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2 EE 3
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        RESULT 6
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C;Accession: B39040
C;Accession: B39040
A;Sicala, S:E; Jones, L.R.
A;Ricala, S:E; Jones, L.R.
A;Ritle: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein A;Reference number: A39040; MUID:91093153; PMID:1985907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rifriedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.3A. 81, 3044-3048, 1984
A;Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricula
A;Reference number: 146886; MUID:84221901; PMID:6328491
hydrogensulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragment) N.Alternate names: bisulfite reductase; desulfofuscidin C.Species: Desulfovibrio thermophilus C.Species: Desulfovibrio thermophilus C.Spate: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998 C.Accession: 311556 R.Feuque, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.; I Biochim. Biophys. Acta 1040, 112-118, 1990 A.A.Title: Purification and characterization of bisulfite reductase (desulfofuscidin) from A.Reference number: S11024; MUID:90335276; PMID:2165817
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C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C;Accession: 146868
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A;Molecule type: protein
A;Residues: 1-7 <CAL>
C;Keywords: phosphoprotein; skeletal muscle
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Matches 2; Conservative
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A; Residues: 1-6 <FAU>
C; Keywords: oxidoreductase
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A; Residues: 1-7 <FRI>
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tocopherol-binding protein, 81K - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996
C;Datession: 229272; MJ: Azzi, A.
R;Nalecz, K.A.; Nalecz, M.J.; Azzi, A.
Eur. J. Biochem. 209, 37-42, 1992
A;Title: Isolation of tocopherol-binding proteins from the cytosol of smooth muscle A;Reference number: S29272; MUID:93011150; PMID:1396710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (strain NI3) (fra aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (5.5 pecies: Corynebacterium flavum C.5 bate: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 19-Dec-1997 C.5 Accession: B47594 R.Follettie, M.T.: Peoples, O.P.: Agoropoulou, C.; Sinskey, A.J.
J. Bacteriol. 175, 4096-4103, 1993 A;Fitle: Gene structure and expression of the Corynebacterium flavum NI3 ask-asd Op A;Reference number: A47594; MUID:93308099; PMID:8100567
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ilarity 100.0%; Pred. No. 2.8e+05;
Conservative 0; Mismatches 0;
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A;Residues: 1-8 <NAL>
A;Experimental source: smooth muscle A7r5 cells
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A.Accession: A61230
A.Molecule type: protein
A.Residues: 1-9 cMCL>
C.Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding protein C.Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound to C.Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in vi C.Superfamily: calsequestrin
C.Superfamily: calsequestrin
C.Keywords: calcium binding; cardiac muscle; glycoprotein; heart; phosphoprotein; skelet
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N;Alternate names: 58K dihydropyridine-binding protein; aspartactin; calmitine; laminin-
S;Species: Rana piplens (northern leopard frog)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C;Accession: A61230
E;McLecod, A.G.; Shen, A.C.Y.; Campbell, K.P.; Michalak, M.; Jorgensen, A.O.
Circ. Res. 69, 344-359, 1991
A;Title: Frog cardiac calsequestrin. Identification, characterization, and subcellular didium.
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                                                                                   C;Species: Kaiware daikon (Japanese radish)
C;Species: Kaiware daikon (Japanese radish)
C;Species: Naiware daikon (Japanese radish)
C;Species: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
C;Data, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
Arch. Biochem. Biophys. 316, 797-802, 1995
A;Title: Four ferredoxins from Japanese radish leaves.
A;Reference number: S69164; MUID:95168867; PMID:7864635
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-8 <OBA>
C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein
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Caldesmon - rabbit (fragment)

Caldesmon - rabbit (fragment)

Cipate: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997

Cipate: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997

Cipate: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997

Cipate: Mornick, T.

Arch. Biochem. Biophys. 288, 538-542, 1991

Aritle: Determination of the phosphorylation sites of smooth muscle caldesm

Arcession: A44873; MUID:91378498; PMID:1898046
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A;Residues: 1-9 <IKE>
A;Experimental source: skeletal myosin
A;Note: sequence extracted from NCBI backbone (NCBIP:63199)
C;Superfamily: caldesmon
                                                                      - Japanese radish (fragment)
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Best Local Similarity 100.C
Matches 2; Conservative
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R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Blochem. 97, 1487-1492, 1985
A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas mon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 1-9 <NAK>
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen o
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N;Contains: fibrinopeptide B
C;Species: Erythrocebus patas (red guenon, hussar)
C;Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
C;Accession: D24.180
R;Nakamura, S; Takenaka, O.; Takahashi, K.
J. Blochem. 97, 1487-1492, 1995
A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas mor
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C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 18-Jun-1993
C;Accession: C60070
C;Accession: C60070
C;Accession: C60070
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C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen
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N;Contains: fibrinopeptide B
C;Species: Macaca fuscata (Japanese macaque)
C;Date: 05-Jun.1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
C;Accession: C24180
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Pred. No. 2.8e+05;
0; Mismatches 0; Indels
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A;Accession: C24180
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A;Accession: D24180
76.9%; brod. No. 2.100.0%; Pred. No. 2.100.0%;
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                       Query Match
Best Local Similarity
Matches 2; Conserv
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Jate G1-69 protein - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Spate: 16-7u1-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C.Accession: PH0108
R.Nikaido, T.: Bradley, D.W.; Pardee, A.B.
Exp. Cell Res. 192, 102-109, 1991
A.Title: Molecular cloning of transcripts that accumulate during the late G1 phase in cu A.Reference number: PH0108, MUID:91078351; PMID:1984406
A.Accession: PH0108
A.Status: preliminary
A.Nolecule type: mRNA
A.Nolecule type: mRNA
A.Residues: 1-9 <NIK>
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                                                                                             Query Match 76.9%; Score 10; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <DES>
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7 EE 8
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PH0108
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 11, 2003, 18:07:35; Search time 2.21649 Seconds (without alignments) 93.563 Million cell updates/sec Run on:

US-09-380-738A-5 13 1 XXXEE 5 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	B13973 ASCHARLE			Ŋ	\sim		Q10997 halocynthia	_	Q05055 tetrahymena		P31859 vipera beru				P80578 hydra atten	P40928 homo sapien		_	_	P41493 sarcophaga		_	P16392 equus cabal		e pinus	73	39 callip	61	æ	σ	P81528 mycobacteri	3714	P81733 leucophaea
SUMMARIES	ID	TRM3 ECOLI		FIBB_ERYPA	FIBB_MACFU	COXA_ONCMY	COXO_RAT	SPI_HALRO	COXA_CANFA	CALM_TETTH	HS9A_RAT	PA2B_VIPBO	BP37_LEUMA	E121_LITRU	EI22_LITRU	PEDI_HYDAT	UHA1_HUMAN	DHSL_ANACY	FIBA_HORSE	FIBB_MANLE	NSK2_SARBU	UC15_MAIZE	ESTJ_MANSE	GR78_HORSE	METK_MAIZE	UN01_PINPS	UNO4_PINPS	ALL1_CALVO	FIBA_EQUAS	IBP4_PIG	UPAB_HUMAN		GAST_MACMU	TRP2_LEUMA
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UF03_MOUSE STANDARD; PRT; 7 AA. P38641; 01-0CT-1994 (Rel. 30, Created) 01-0CT-1994 (Rel. 31, Last sequence update) 01-FEB-1995 (Rel. 31, Last annotation update)

RESULT 2
UF03_MOUSE
ID UF03_MO
AC P38641;
DT 01-0CTDT 01-0CTDT 01-FEB-

10 76.9 18 1 OBP_LYMDI P34173 Jymantria d	ALIGNMENTS T 1	ECOLI 3; N-1990 (N-1990 (C-1998 (TraM protein (Fragment). TRAM. Bscherichia coli. Plasmid IncFII R100. Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Rscherichia. NCBI_Tax1D=562;	N.A. shioka Y., Ohtsubo E.; and characterization of the products from the tranof plasmid R100."; 170:274-2757(1988). BRANSFER GELLS FOR THE EXCHANGE OF PLASMID DNA. R LOCATION: Cytoplasmic. TO TRAM PROTEIN OF OTHER PLASMIDS.	his SWISS-PROT entry is copyricated the European Bloinformatics Ins se by non-profit institutio odified and this statement is ntities requires a license agr r send an email to license@fisb	MBL; M20941; -; NOT_ANNOTATED_CDS. IR; A32014; A32014. Onjugation; Plasmid; DNA-binding. ON_TER EQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;	Ouery Match 76.9%; Score 10; DB 1; Length 5; Best Local Similarity 100.0%; Pred. No. 1.1e+05; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	4 BE 5 4 BE 5
888888844444 450788013844	RESULT	M3			CCC CCC CCC CCC CCC CCC CCC CCC CCC CC		Query M Best Lo Matches	QY Db

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TISSUE-Liver;
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P80328;
                                                        FIBB_MACFU
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2 EE
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                                            FIBB_MACFU
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                                                                   qq
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Nakamura S., Takenaka O., Takehashi K.;
Nakamura S., Takenaka O., Takehashi K.;
Nakibiriopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (Erythrocebus patas): their amino acid sequences, restricted mutations, and amolecular phylogeny for macaques, J. Blochem. 97:1487-1492(1985).
-!- FUNCTION: FIBRINGGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-i- MISCELLANGOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMEIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                                                                                                                                                                                                                     Gaps
                                                                                       Mus musculus (Mouse).
Sakaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                        Erythrocebus patas (Red guenon) (Hussar).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
                                                                                                                                                                                                           76.9%; Score 10; DB 1; Length 7; 100.0%; Pred. No. 1.1e+05;
                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69FE7879C732CB1B CRC64;
                                                                                                                                                                                     7 AA; 842 MW; 6AA72B1DDB1B1180 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.9%; Score 10; DB 1; L
100.0%; Pred. No. 1.1e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; D24180; D24180.
InterPro; IPR002181; Fibrinogen_C.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIBRINOPEPTIDE B.
                                                                                                                                                                                                                                                                                                                                         9 AA.
                                                                                                                                                                                                                       ; Pred. No. 1.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae; Erythrocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AA; 1020 MW;
                                                                                                                                                                                                                       Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                               FISSUE=Fibroblast;
                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGREGATION.
                                                                                                                                                                                                                                                                                                                                         FIBB_ERYPA
P19346;
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SEQUENCE
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Nakamura S., Takenaka O., Takahashi K.;
Nakamura S., Takenaka O., Takahashi K.;
Pibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (Erythrocebus patas): their amino acid sequences, restricted mutations, and a molecular phylogeny for macaques, guenons, and baboons.";
I Blochem 97:1487-1492(1985)
I Blochem 97:1487-1492(1985)
I POLYMERIZE INTO FIBRIN GEN ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-!- MISCELLANDOUS: CONVERSION OF FIBRINOSEN TO FIBRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase isolated from rainbow trout."; Eur. J. Biochem. 221:1111-1116(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryotai Metazoa; Chordata; Craniata; Vertebratai; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                               01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1900 (Rel. 11, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 10; DB 1; Length 9; Pred. No. 1.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA; 1038 MW; 69FE65B9C735BB1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; C24180; C24180.
InterPro; IPR002181; Fibrinogen_C.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIBRINOPEPTIDE B.
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                                                                                                                                                                                      Macaca fuscata fuscata (Japanese macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94237150; PubMed=8181469;
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-85289140; PubMed-3928610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blood coagulation; Plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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STANDARD;
                                                                                                                                                                                                                                                                     Cercopithecinae; Macaca.
NCBL_TaxID=9543;
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Best Local Similarity
'-hes 2; Conserv?
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Indels

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Conservative

Matches

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-!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONBRIAL ELECTRON TRANSPORT.-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + 0(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Wistar; TISSUE-Liver, and Heart;
MEDLINE=95224529; PubMed=7601105;
Schaegger H., Noack H., Halangk W., Brandt U., von Jagow G.;
"Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adult liver isoform.;

Eur. J. Biochem. 230:235-241(1995).

-!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-Jycohrome coxidase polypeptide VIIC, mitochondrial (EC 1.9.3.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY. Oxidoreductase, Mitochondrion. NON_TER 10\ 10
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0
                                                                  -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
PIR; S43625; S43625.
Oxidoreductase; Heme; Mitochondrion; Inner membrane.
                                                                                                                                                                                                   / Match 76.9%; Score 10; DB 1; Length 10; Local Similarity 100.0%; Pred. No. 7.7e+02; les 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.9%; Score 10; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 7.7e+02; Matches 2; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA; 1117 MW; 126DE767687B1B0B CRC64;
                                                                                                                                                                10 AA; 1144 MW; C535C5B1AB02C33D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            10 AA
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                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (VIIIA) (Fragment). COX7C OR COX7C1.
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P80432;
                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                        Query Match
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DT 01-0C
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-!- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Čhordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBL_TaxID=9615;
                                                                  Shishikura F., Abe T., Ohtake S.-I., Tanaka K.; "Purification and characterization of a 58,000-Da proteinase inhibitor from the hemolymph of a solitary ascidian, Halocynthia
                                                                                                                                                                                                                                                                                     ;
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-!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.9%; Score 10; DB 1; Length 11; 100.0%; Pred. No. 8.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                       Query Match 76.9%; Score 10; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 7.7e+02; Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                             -i- SUBUNIT: MONOMER.
-i- SIMILARITY: BELCOGS TO THE SERPIN FAMILY.
InterPro: IPRO00215; Serpin.
PROSITE; PS00284; SERPIN; PARTIAL.
Serpin; Serine protease inhibitor; Glycoprotein; Plasma.
                                                                                                                                                                                                                               10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxidoreductase; Heme; Mitochondrion; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              11 AA
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                    MEDLINE=96321313; PubMed=8759295;
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InterPro; IPR003204; Cyt_c_ox5A.
Pfam; PF02284; COX5A; 1.
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Best Local Similarity 100.(
Matches 2; Conservative
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Canis familiaris (Dog).
                                       TISSUE-Hemolymph;
NCBI_TaxID=7729;
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P99501:
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                          SEQUENCE.
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CALM_TETTH

RESULT 9

us-09-380-738a-5.rsp

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(BY SIMILARITY)
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BP37_LEUMA
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                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                  Katoh M., Hirono M., Takemasa T., Kimura M., Watanabe Y.;
"A micronucleus-specific sequence exists in the 5'-upstream region of calmodulin gene in Terrahymena thermophila.";
Nucleic Acids Res. 21.2409-244(1993).
Nucleic Acids Res. 21.2409-244(1993).
ENZYMES BY CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
                     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calmodulin (Fragment).
Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Sprague-Dawley; TISSUE-Liver; MEDLINE=21589773; PubMed=11732320; Langer T., Fasold H.; Langer T., Fasold H.; "Isolation and quantification of the heat shock protein 90 alpha and beta isoforms from rat liver."; Protoplasma 218:54-56(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                        MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING SITES.
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                                                                                                                                                                                                                                                                                                     SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 AA; 1393 MW; 83F31CD443DB1B01 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heat shock protein HSP 90-alpha (Fragment).
12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D127/4; BARVALDET, AND TREEPERS; IPRO02048; EF-HAND; PARITAL. PROSITE; PS00018; EF-HAND; PARITAL. Calcium-binding; Repeat; Acetylation. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
 PRT;
                                                                                                                                                         MEDLINE=93281388; PubMed=8506136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.9%;
llarity 100.0%;
Conservative 0
STANDARD;
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les 2; Conserv
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                                                                                                                 NCBI_TaxID=5911;
CALM_TETTH
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SEQUENCE
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P82995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The properties of a toxic A2 phospholipase isolated from the venom of viperties of a toxic A2 phospholipase isolated from the venom of vipertiae of a toxic A2 phospholipase isolated from the venom of viperidae of a toxic A2 phospholipase isolated from the venom of viperidae of a toxic A2 phospholipase isolated from the venom of viperidae of a toxic A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholipase A2 phospholi
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                                                                        -:- SIMILARITI: DELCONO.
InterPro; IPPRO11404; HSp90.
PROSITE; PS00298; HSP90; PARTIAL.
Chaperone; ATP-binding; Heat shock; Phosphorylation.
PHOSPHORYLATION (BY DS-DNA KINASE) (BY
                                                                                                                                                                                                                                                SIMILARITY).
PHOSPHORYLATION (BY DS-DNA KINASE) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Vipera.
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0
-1- SUBUNIT: Homodimer (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase R2, basic (EC 3.1.1.4) (Phosphatidylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12;
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                                                                                                                                                                                                                                                                                                                                                                                              12 AA; 1432 MW; DE47C322CAB6C1B6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.9%; Score 10; DB 1; L4 100.0%; Pred. No. 9.3e+02; tive 0; Mismatches 0;
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100.0%; Pred. No. 2...
0; Mismatches
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MEDLINE=74128698; PubMed=4206446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vipera berus orientalis (Viper).
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Rest Local Similarity

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P31859;
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P81754;
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SEQUENCE
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
16-027-2001 (Rel. 40, Last annotation update)
16-027-2001 (Rel. 40, Last annotation update)
16-027-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                           Muren J.E., Naessel D.R.; "Seven tachykinin-related peptides isolated from the brain of the madeira cockroach; evidence for tissue-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Ambhliai, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae, Pelodryadinae, Litoria.
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C1808EF326F57322 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides 18:7-15(1997).
--- TISSUE SPECIFICITY: BRAIN.
--- MASS SPECTROMETRY: WW=1435_77; METHOD=MALDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-UUN-2002 (Rel. 41, Created)
15-UUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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-!- SUBCELLUIAR LOCATION: SECRETED.
Amphibian skin; Amidation. AMIDAT
MOD_RES 13 13 AMIDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Electrin 2.1.
Litoria rubella (Desert tree frog).
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                                                                                                                                                                                                                                                                                               TISSUE=Brain;
MEDLINE=97269266; PubMed=9114447;
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les 2; Conserv
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15-JUN-2002 (
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P82098;
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E121_LITRU
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EI22_LITRU
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                                                                                                                   Wabhitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydra attenuata (Hydra) (Hydra vulgaris).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
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                                                                                                                                                                                                                                                       76.9%; Score 10; DB 1; Length 13; 100.0%; Pred. No. 1e+03; tive 0; Mismatches 0; Indels
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1e+03;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               13 AA
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                                                                                                                                                                                                                  AMIDATION
                                                                                                                                                                        Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLUIAR LOCATION: SECRETED.
Amphibian skin; Amidation.
13 13 13 AMIDAT
Electrin 2.2.
Litoria rubella (Desert tree frog).
                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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nes 2; Conservative
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                                                                                                         TISSUE-Skin secretion;
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les 2; Conserv
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                                                                NCBI_TaxID=104895
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GenCore version 5.1,3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 11, 2003, 18:13:41; Search time 5.61856 Seconds (without alignments) 183.363 Million cell updates/sec Run on:

US-09-380-738A-5 13

1 XXXEE 5 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

671580 Total number of hits satisfying chosen parameters:

671580 seqs, 206047115 residues

Searched:

seq length: 0 seq length: 2000000000 Minimum DB & Maximum DB &

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

Database :

SPTREMBL_21:*

sp_archea:* sp_bacteria:*

sp_unclassified:* sp_fungi:*
sp_human:*
sp_invertebrate:* sp_vertebrate:* sp_rvirus:*
sp_bacteriap:* sp_organelle:* sp_plant:* sp_rodent:* sp_mammal:* sp_virus:* sp_phage:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

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æ	Query Match Le	76.9	6.92	76.9	6.92	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9		6.9/	6.92
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76.9	76.9	76.9 10	76.9	76.9	6.9	6.9	76.9	76.9	6.92	6.92	76.9	6.92	6.92	76.9	76.9	76.9	76.9	6.92	76.9	6.97	6.9	76.9	6.9	6.97	6.9	76.9	6.97	6.92	
		19 10																							•			45 10	

ALIGNMENTS

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"Characterization of genomic clones specifying rabbit alpha- and beta-ventricular myosin heavy chains.";
Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
EMBL; K01698; AAA31415.1;
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                            01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01.DEC-2001 (TrEMBLrel. 19, Last annotation update)
Alpha-myosin heavy chain (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                      MEDLINE-84221901; PubMed-6328491;
Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovcic S.,
Rabinowitz M.;
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                                                                                                                                                                                                                                                                                                                7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
    PRT;
PRELIMINARY;
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SEQUENCE
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Query Match
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STRAIN=GLA121, AND GLA124;
MEDLINE=21561594; PubMed=11703875;
Lessios H.A., Garrido M.J., Kessing B.D.;
"Demographic history of Diadema antillarum, a keystone herbivore on Caribbean reefs.";
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
                                                                   Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
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                                                                                                                                                Lessios H.A., Kessing B.D., Pearse J.S.;
"Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema.";
Evolution 55:955-975(2001).
EMBL; AY01959; AAL33852.1; -.
                                                       Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
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Mismatches 0; Indels
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EMBL: AY012931; AAL33845.1; -.
EMBL: AY012932; AAL33846.1; -.
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Cytochrome oxidase subunit II (Fragment).
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STRAIN-GLA121, AND GLA124;
MEDLINE-21323357; Pubmed=11430656;
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MEDLINE=21323357; PubMed=11430656;
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                                    Diadema paucispinum.
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Matches 2; Conserv
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                                                                                          NCBI_TaxID=145530;
                                                                                                                 SEQUENCE FROM N.A.
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Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
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Echinoidea, Euechinoidea, Diadematacea, Diadematoida, Diadematidae,
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STRAIN=C15, D3, D5, D6, CC66, G123, DM1, DM3, AND DM71;
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EMBL; AY012796; AAL33821.1;

EMBL; AX012799; AAL33822.1;

EMBL; AX012803; AAL33823.1;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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EMBL, AY012834; AAL33828.1; -.
Mitochondrion. 1
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STRAIN=C15, D3, D5, D6, CC66, G123, DM1, DM3, AND DM71;
MEDLINE=21561594; PubMed=11703875;
Lessios H.A., Garrido M.J., Kessing B.D.;
"Demographic history of Diadema antillarum, a keystone herbivore on
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Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
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                     Lessios H.A., Kessing B.D., Pearse J.S.;
"Population structure and speciation in tropical seas: global
phylogeography of the sea urchin Diadema.";
Evolution 55:955-975(2001).
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EMBL; AY012008; AAL33837.1; -

EMBL; AY012911; AAL33838.1; -

EMBL; AY012914; AAL33840.1; -

EMBL; AY012919; AAL33847.1; -

EMBL; AY012940; AAL33847.1; -

EMBL; AY012950; AAL33847.1; -

EMBL; AY012951; AAL33847.1; -

EMBL; AY012951; AAL33850.1; -

EMBL; AY012951; AAL33851.1; -

EMBL; AY012951; AAL33851.1; -
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8 AA; 1037 MW; 701B173B46DDC2D3 CRC64;
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MEDLINE=21323357; PubMed=11430656;
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SEQUENCE FROM N.A.
STRAIN=DP751, SA2, SA7, SA10, GSA1, GSA3, GSA4, DOK17, AND DOK105;
X MEDINEL-21323357; Pubmed=11430656;
A Lessios H.A., Kessing B.D., Pearse J.S.;
Thylogeography of the sea urchin Diadema.";
Evolution 55:955-975(2001).
IL Evolution 55:955-975(2001).
REMBL; AY013086; AAL33860.1; -
REMBL; AY013089; AAL33861.1; -
REMBL; AY013089; AAL33864.1; -
REMBL; AY013099; AAL33864.1; -
REMBL; AY013099; AAL33864.1; -
REMBL; AY013102; AAL33867.1; -
REMBL; AY013102; AAL33867.1; -
REMBL; AY013102; AAL33869.1; -
REMBL; AY013102; AAL33869.1; -
REMBL; AY0131013; AAL33869.1; -
REMBL; AY0131013; AAL33869.1; -
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MEDLINE=96189275; PubMed=8605312;
Joshi C.P., Kumar S., Nguyen H.T.;
"Application of modified differential display technique for cloning and sequencing of the 3' region from three putative members of wheat HSP70 gene family.";
Plant Mol. Biol. 30:641-646(1996).
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Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
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                                                             Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
  8 AA
                                                                                                             Cytochrome oxidase subunit II (Fragment).
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                                      01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20,
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Matches 2; Conservative
PRELIMINARY;
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01-MAY-2000 (TrEMBLrel. 21, Last sequence update)
01-MAY-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CALDESMON-PHOSPHORYLATION site (Fragment).
OTYCLOLAGUS cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi;
Archosauria; Aves; Neognathae; Gruiformes; Rallidae; Fulica.
NCBL_TaxID=156758;
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Shapiro L.H., Dumbacher J.P.;
"Adenylate kinase intron 5: a new nuclear locus for avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.9%; Score 10; DB 13; Length 8; ilarity 100.0%; Pred. No. 6.7e+05; Conservative 0; Mismatches 0; Indels
                                                                                         Length 8;
                                                                                      'Match 76.9%; Score 10; DB 10; Length 8; Local Similarity 100.0%; Pred. No. 6.7e+05; nes 2; Conservative 0; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Adenylate kinase (Fragment).
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SEQUENCE 8 AA; 886 MW; 71B2CB1B10532768 CRC64;
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MEDLINE=91378498; Pubmed=1898046;
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Auk 118:248-255(2001).
EMBL; AF307898; AAK43537.1; -.
EMBL; L41507; AAB02333.1; -. EMBL; L41505; AAB02331.1; -. EMBL; L41506; AAB02332.1; -.
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Matches 2, Conserv
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Score 10; DB 6; Length 9;

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MEDLINE-215194; PubMed-11703875;
Lessios H.A., Garrido M.J., Kessing B.D.;
"Demographic history of Diadema antillarum, a keystone herbivore on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diadema mexicanum.
Mitochondrion.
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
Diadema.
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                                                                                                                                                                                                                                                                                                                      Lessios H.A., Kessing B.D., Pearse J.S., population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema."; Evolution 55:955-975(2001).
                                                                                                                                                                                                              Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
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EMBL: AY012858; AAL33832.2;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Cytochrome oxidase subunit II (Fragment).
                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Cytochrome oxidase subunit II (Fragment).
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9 AA; 1115 MW; EDF8DB1B173B46CA CRC64;
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MEDLINE-21323357; PubMed=11430656;
Lessios H.A., Kessing B.D., Pearse J.S.;
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01-MAR-2002 (TrEMBLrel. 20, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
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'..hes 2; Conserve
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STRAIN=CC70, AND CC117;
MEDLINE=218561594; PubMed=11703875;
Lessios H.A., Garrido M.J., Kessing B.D.;
"Demographic history of Diadema antillarum, a keystone herbivore on Caribbean reefs.";
                                                                                                                                 MEDLINE=21561594; PubMed=11703875;
Lessios H.A., Garrido M.J., Kessing B.D.,;
"Demographic history of Diadema antillarum, a keystone herbivore on
Carlibbean reefs.";
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Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
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STRAIN=CCTO, AND CC117;
MEDLINE=2123357; Pubmed=11430656;
Lessios H.A., Kessing B.D., Pearse J.S.;
"Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema.";
Evolution S5:955-975(2001).
"Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema.";
Evolution 55:955-975(2001).
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EMBL, AV012941; AAL33848.1;
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EMBL: AY012920; AAL33843.1; -
EMBL: AY012921; AAL33844.1; -
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9 AA; 1174 MW; 2B73173B46DDC2D3 CRC64;
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                                                                                            SEQUENCE FROM N.A.
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Q8W8X4
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Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
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MEDLINE=21561594; PUMGd=11703875;
Lessios H.A., Garrido M.J., Kessing B.D.;
"Demographic history of Diadema antillarum, a keystone herbivore on
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Diadematacea; Diadematoida; Diadematidae;
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MEDLINE=21323357; PubMed=11430656;
Lessios H.A., Kessing B.D., Pearse J.S.;
"Population structure and speciation in tropical seas: global phylogeography of the sea urchin Diadema.";
Evolution 55:955-975(2001).
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Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001)
EMBL, AY012853, AAL33827.1; -.
EMBL, AY012855; AAL33829.1; -.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                          01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20,
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0; Gaps 0; Ouery Match 76.9%; Score 10; DB 8; Length 9; Best Local Similarity 100.0%; Pred. No. 6.7e+05; Matches 2; Conservative 0; Mismatches 0; Indels δy

Search completed: February 11, 2003, 18:19:47 Job time: 6.61856 secs

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